

STIC-Biotech/ChemLib

169937

From: Myers, Carla
Sent: Wednesday, October 05, 2005 4:35 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 09/887941

Please do an oligomer search in commercial and interference files for fragments of SEQ ID NO: 1-10 -
please limit the search results to
nucleic acids of a length of 50 nucleotides or less.

please provide a printout of the first 40 results.

The CRF has been entered; http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=09887941

Thank you

Carla Myers
AU 1634
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Mailbox: REM 2C70
571-272-0747

RECEIVED
OCT -5 2005
STIC/BIOTECH. DIVISION
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 : Search time 330.119 Seconds
(without alignments)
4536.068 Million cell updates/sec

Title: US-09-887-941B-10

Perfect score: 215
Sequence: 1 acgcggcgacacgtctctca.....attctgtacgcgcgcgtgc 215

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapept 60.0

Searched: 8443130 seqs, 3482420727 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
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7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
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20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	8.4	25	22	US-10-719-956-430481 Sequence 430481,
2	16	7.4	25	21	US-10-719-900-335376 Sequence 335376,
3	16	7.4	25	21	US-10-719-900-379840 Sequence 379840,
4	16	7.4	25	21	US-10-719-900-567937 Sequence 567937,
5	16	7.4	25	24	US-11-036-317-139770 Sequence 139770,
6	16	7.4	25	24	US-11-036-317-615245 Sequence 615245,
7	16	7.4	25	24	US-11-036-317-615975 Sequence 615975,

8	15	7.0	25	21	US-10-719-900-278239 Sequence 278239,
9	15	7.0	25	21	US-10-719-900-806136 Sequence 806136,
10	15	7.0	25	21	US-10-809-189-14636 Sequence 14636, A
11	15	7.0	25	21	US-10-809-189-14653 Sequence 14653, A
12	15	7.0	25	21	US-10-956-157-130791 Sequence 130791,
13	15	7.0	25	21	US-10-956-157-134955 Sequence 134955,
14	15	7.0	25	21	US-10-956-157-137770 Sequence 137770,
15	15	7.0	25	21	US-10-956-157-150085 Sequence 150085,
16	15	7.0	25	21	US-10-956-157-150649 Sequence 150649,
17	15	7.0	25	21	US-10-956-157-164027 Sequence 164027,
18	15	7.0	25	21	US-10-956-157-169794 Sequence 169794,
19	15	7.0	25	21	US-10-956-157-177304 Sequence 177304,
20	15	7.0	25	21	US-10-956-157-181926 Sequence 181926,
21	15	7.0	25	21	US-10-956-157-218881 Sequence 218881,
22	15	7.0	25	21	US-10-956-157-218881 Sequence 218881,
23	15	7.0	25	21	US-10-956-157-218881 Sequence 218881,
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37	15	7.0	25	21	US-10-956-157-218881 Sequence 218881,
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39	15	7.0	25	21	US-10-956-157-218881 Sequence 218881,
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41	15	7.0	25	21	US-10-956-157-218881 Sequence 218881,
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c 81 14 6.5 25 22 US-10-719-956-88069, A
c 82 14 6.5 25 22 US-10-719-956-471310,
c 83 14 6.5 25 22 US-10-719-956-417985,
c 84 14 6.5 25 22 US-10-719-956-426757,
c 85 14 6.5 25 22 US-10-719-956-471887,
c 86 14 6.5 25 22 US-11-036-317-34756,
c 87 14 6.5 25 24 US-11-036-317-126909,
c 88 14 6.5 25 24 US-11-036-317-145174,
c 89 14 6.5 25 24 US-11-036-317-180236,
c 90 14 6.5 25 24 US-11-036-317-197701,
c 91 14 6.5 25 24 US-11-036-317-256553,
c 92 14 6.5 25 24 US-11-036-317-290634,
c 93 14 6.5 25 24 US-11-036-317-296034,
c 94 14 6.5 25 24 US-11-036-317-321487,
c 95 14 6.5 25 24 US-11-036-317-411048,
c 96 14 6.5 25 24 US-11-036-317-473214,
c 97 14 6.5 25 24 US-11-036-317-483701,
c 98 14 6.5 25 24 US-11-036-317-665577,
c 99 14 6.5 25 24 US-11-036-317-666848,
c 100 14 6.5 25 24 US-11-036-317-700492,

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ALIGNMENTS

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RESULT 1
US-10-719-956-430481
; Sequence 430481, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430481
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-430481

Query Match      8.4%; Score 18; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 184 GTTGCTGTGTCATTGT 201
Db 4 GTTGCTGTGTCATTGT 21

RESULT 2
US-10-719-900-335376
; Sequence 335376, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 335376
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-335376

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Query Match      7.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 177 GAGTTTCGTTGCTGTG 192
Db 7 GAGTTTCGTTGCTGTG 22

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```

RESULT 3
US-10-719-900-379840/c
; Sequence 379840, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 379840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-379840

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```

Query Match      7.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Oy 6 GGCACAGTCTTCAG 21
Db 16 GGCACAGTCTTCAG 1

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RESULT 4
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; Sequence 567937, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 567937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-567937

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```

Query Match      7.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 6 GGCACAGTCTTCAG 21
Db 19 GGCACAGTCTTCAG 4

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RESULT 5
US-11-036-317-139770/c
; Sequence 139770, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 : Search time 65.9759 Seconds
(without alignments)
5332.244 Million cell updates/sec

Title: US-09-887-941B-10

Perfect score: 215
Sequence: 1 aecgcgcgcacagctctca.....atttgtgagacgcgcgcgc 215

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:*

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6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	15	7.0	25	4	US-09-396-196G-14636 Sequence 14636, A
2	15	7.0	25	4	US-09-396-196G-14653 Sequence 14653, A
3	15	7.0	25	4	US-09-428-082B-379 Sequence 379, App
4	15	7.0	50	4	US-08-030-175-31 Sequence 31, App1
5	14	6.5	18	2	US-08-350-260A-564 Sequence 564, App
6	14	6.5	18	4	US-09-104-337A-564 Sequence 564, App
7	14	6.5	25	4	US-09-396-196G-98690 Sequence 98690, A
8	14	6.5	25	4	US-09-396-196G-98691 Sequence 98691, A
9	14	6.5	39	2	US-08-350-260A-582 Sequence 582, App
10	14	6.5	39	4	US-09-104-337A-582 Sequence 582, App
11	14	6.5	41	2	US-08-350-260A-580 Sequence 580, App
12	14	6.5	41	2	US-08-350-260A-581 Sequence 581, App
13	14	6.5	41	2	US-08-350-260A-585 Sequence 585, App
14	14	6.5	41	2	US-08-350-260A-586 Sequence 586, App
15	14	6.5	41	2	US-08-350-260A-588 Sequence 588, App
16	14	6.5	41	2	US-08-350-260A-589 Sequence 589, App
17	14	6.5	41	2	US-09-104-337A-579 Sequence 579, App
18	14	6.5	41	4	US-09-104-337A-580 Sequence 580, App
19	14	6.5	41	4	US-09-104-337A-581 Sequence 581, App
20	14	6.5	41	4	US-09-104-337A-585 Sequence 585, App
21	14	6.5	41	4	US-09-104-337A-586 Sequence 586, App
22	14	6.5	41	4	US-09-104-337A-588 Sequence 588, App
23	14	6.5	41	4	US-09-104-337A-589 Sequence 589, App
24	14	6.5	41	4	US-08-350-260A-557 Sequence 557, App
25	14	6.5	44	4	US-08-350-260A-558 Sequence 558, App
26	14	6.5	44	2	US-08-350-260A-559 Sequence 559, App
27	14	6.5	44	2	US-08-350-260A-559 Sequence 559, App

28	14	6.5	44	2	US-08-350-260A-560 Sequence 560, App
29	14	6.5	44	2	US-08-350-260A-561 Sequence 561, App
30	14	6.5	44	2	US-08-350-260A-562 Sequence 562, App
31	14	6.5	44	2	US-08-350-260A-583 Sequence 583, App
32	14	6.5	44	2	US-08-350-260A-584 Sequence 584, App
33	14	6.5	44	2	US-08-350-260A-587 Sequence 587, App
34	14	6.5	44	2	US-09-104-337A-557 Sequence 557, App
35	14	6.5	44	4	US-09-104-337A-558 Sequence 558, App
36	14	6.5	44	4	US-09-104-337A-559 Sequence 559, App
37	14	6.5	44	4	US-09-104-337A-560 Sequence 560, App
38	14	6.5	44	4	US-09-104-337A-561 Sequence 561, App
39	14	6.5	44	4	US-09-104-337A-562 Sequence 562, App
40	14	6.5	44	4	US-09-104-337A-583 Sequence 583, App
41	14	6.5	44	4	US-09-104-337A-584 Sequence 584, App
42	14	6.5	44	4	US-09-104-337A-587 Sequence 587, App
43	13	6.0	17	3	US-09-096-731A-23 Sequence 23, App1
44	13	6.0	17	3	US-09-096-731A-23 Sequence 23, App1
45	13	6.0	19	3	US-09-262-773-24 Sequence 24, App1
46	13	6.0	19	3	US-09-262-773-24 Sequence 24, App1
47	13	6.0	21	3	US-09-856-072A-8 Sequence 8, App1
48	13	6.0	21	3	US-09-856-072A-8 Sequence 8, App1
49	13	6.0	25	4	US-09-396-196G-14760 Sequence 14760, A
50	13	6.0	25	4	US-09-396-196G-70565 Sequence 70565, A
51	13	6.0	25	4	US-09-396-196G-113519 Sequence 113519, A
52	13	6.0	25	4	US-09-396-196G-113520 Sequence 113520, A
53	13	6.0	25	4	US-09-396-196G-113521 Sequence 113521, A
54	13	6.0	25	4	US-09-396-196G-118227 Sequence 118227, A
55	13	6.0	25	4	US-09-396-196G-118228 Sequence 118228, A
56	13	6.0	25	4	US-09-396-196G-118239 Sequence 118239, A
57	13	6.0	25	4	US-09-396-196G-118240 Sequence 118240, A
58	13	6.0	42	1	US-07-834-539A-14 Sequence 14, App1
59	13	6.0	42	1	US-08-053-131-22 Sequence 22, App1
60	13	6.0	42	1	US-08-645-641-22 Sequence 22, App1
61	13	6.0	42	1	US-07-853-408B-22 Sequence 22, App1
62	13	6.0	42	1	US-08-096-762-22 Sequence 22, App1
63	13	6.0	42	2	US-08-800-353-14 Sequence 14, App1
64	13	6.0	42	2	US-08-308-865-22 Sequence 22, App1
65	13	6.0	42	3	US-09-042-353-190 Sequence 190, App1
66	13	6.0	42	3	US-08-758-417A-38 Sequence 38, App1
67	13	6.0	42	5	PCT-US92-06185-14 Sequence 14, App1
68	13	6.0	42	5	PCT-US92-10983-22 Sequence 22, App1
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70	13	6.0	45	2	US-08-350-260A-546 Sequence 546, App
71	13	6.0	45	2	US-08-350-260A-547 Sequence 547, App
72	13	6.0	45	2	US-08-350-260A-548 Sequence 548, App
73	13	6.0	45	4	US-09-104-337A-545 Sequence 545, App
74	13	6.0	45	4	US-09-104-337A-546 Sequence 546, App
75	13	6.0	45	4	US-09-104-337A-547 Sequence 547, App
76	13	6.0	45	4	US-09-104-337A-548 Sequence 548, App
77	13	6.0	15	1	US-08-111-076-17 Sequence 17, App1
78	12	5.6	15	1	US-08-398-305-17 Sequence 17, App1
79	12	5.6	15	1	US-08-705-225-17 Sequence 17, App1
80	12	5.6	15	4	US-09-641-690A-5 Sequence 5, App1
81	12	5.6	15	4	US-09-798-689-20 Sequence 20, App1
82	12	5.6	17	1	US-08-640-378-22 Sequence 22, App1
83	12	5.6	17	1	US-08-298-886-4 Sequence 4, App1
84	12	5.6	17	4	US-09-076-776-9 Sequence 9, App1
85	12	5.6	17	4	US-09-999-672-4 Sequence 4, App1
86	12	5.6	18	1	US-08-013-801-4 Sequence 4, App1
87	12	5.6	18	1	US-08-072-065-13 Sequence 13, App1
88	12	5.6	18	1	US-08-212-123-4 Sequence 4, App1
89	12	5.6	18	1	US-08-064-693-13 Sequence 13, App1
90	12	5.6	18	1	US-08-430-411-4 Sequence 4, App1
91	12	5.6	18	1	US-08-470-366-4 Sequence 4, App1
92	12	5.6	18	1	US-08-466-822-4 Sequence 4, App1
93	12	5.6	18	2	US-08-704-504-4 Sequence 4, App1
94	12	5.6	18	2	US-08-885-366-13 Sequence 13, App1
95	12	5.6	18	3	US-09-223-344-4 Sequence 4, App1
96	12	5.6	18	3	US-09-425-033A-4 Sequence 4, App1
97	12	5.6	18	3	US-10-196-460-4 Sequence 4, App1
98	12	5.6	18	5	PCT-US93-04774-13 Sequence 13, App1
99	12	5.6	18	5	PCT-US94-01235-4 Sequence 4, App1
100	12	5.6	18	5	PCT-US95-03125-4 Sequence 4, App1

ALIGNMENTS

RESULT 1

US-09-396-196G-14636
; Sequence 14636, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14636
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14636

Query Match

Best Local Similarity 7.0%; Score 15; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AAACATAGCTGTCC 69
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DB 2 AAACATAGCTGTCC 16

RESULT 2

US-09-396-196G-14653
; Sequence 14653, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14653
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14653

Query Match

Best Local Similarity 7.0%; Score 15; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AAACATAGCTGTCC 69
|||||
DB 5 AAACATAGCTGTCC 19

RESULT 3

US-09-428-082B-379/c
; Sequence 379, Application US/09428082B
; Patent No. 6660843

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUN-FA
APPLICANT: CHESTNAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 379
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TMP-TMP-FC
US-09-428-082B-379

Query Match

Best Local Similarity 7.0%; Score 15; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 CACCGCTCCACGAG 130
|||||
DB 28 CACCGCTCCACGAG 14

RESULT 4

US-08-030-175-31/c
; Sequence 31, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:

APPLICANT: Gorman, Scott D.
APPLICANT: Clark, Michael R.
APPLICANT: Cobbold, Stephen P.
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
STREET: 555 13TH ST., NW Suite 701 East
CITY: Washington
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 KB storage
COMPUTER: IBM AT compatible
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
SOFTWARE: WordPerfect 5.0 (Dos text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991

ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 1495.43 Seconds
(without alignments)
5472.564 Million cell updates/sec

Title: US-09-887-941B-10

Perfect score: 215
Sequence: 1 acgcgcgcacagctcttca.....attctgtgagcgcgctgc 215

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0
Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6.5	43	2	BE373472	BE373472 601225842
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4	6.0	42	8	B2379922	B2379922 SALK 1142
5	6.0	43	9	AL756095	AL756095 Arabidops
6	6.0	46	8	A2304027	A2304027 IM0003F12
7	6.0	47	8	A2769488	A2769488 IM0570F15
8	6.0	47	8	A2477112	A2477112 IM0296L20
9	5.6	22	8	A2844206	A2844206 2M0143111
10	5.6	23	8	AM064435	AM064435 SP1032 KR
11	5.6	26	8	A2595068	A2595068 IM0447N20
12	5.6	24	2	AM064435	AM064435 SP1032 KR
13	5.6	26	8	A2447253	A2447253 IM0244N24
14	5.6	29	8	A2980931	A2980931 2M0258R08
15	5.6	30	8	CL521423	CL521423 SAL2B05 F
16	5.6	30	2	BE290626	BE290626 601088341
17	5.6	33	2	BE290626	BE290626 601088341
18	5.6	34	1	AAB71250	AAB71250 VQ33a02.r
19	5.6	35	8	BH910671	BH910671 SALK 0610
20	5.6	36	4	BM396303	BM396303 Arabidops
21	5.6	37	4	BM396303	BM396303 5009-0-2-
22	5.6	37	8	A2794097	A2794097 2M0047P11
23	5.6	37	8	BH861700	BH861700 SALK 0878
24	5.6	38	7	R89825	R89825 YP90a08 .st
		38	8	BH810085	BH810085 SALK 0406
		40	9	BX290497	BX290497 Arabidops

25	5.6	47	8	CC035488	CC035488 3591.1 75
26	5.6	48	8	B2663841	B2663841 SALK_0274
27	5.6	48	8	CC020635	CC020635 3591.1-20
28	5.6	48	8	BX891978	BX891978 Arabidops
29	5.6	49	6	CB213391	CB213391 OML03671
30	5.6	50	1	AU102678	AU102678 AU102678
31	5.6	50	1	AU103071	AU103071 AU103071
32	5.6	50	1	AU104420	AU104420 AU104420
33	5.6	50	1	AU104421	AU104421 AU104421
34	5.6	50	1	AU106547	AU106547 AU106547
35	5.6	50	1	AU106549	AU106549 AU106549
36	5.6	50	1	AU106550	AU106550 AU106550
37	5.6	50	1	AU106551	AU106551 AU106551
38	5.6	50	1	AU107157	AU107157 AU107157
39	5.6	50	1	AU107157	AU107157 AU107157
40	5.6	50	1	BX662020	BX662020 Arabidops
41	5.1	21	8	AZ309054	AZ309054 IM0012A18
42	5.1	22	8	BG928008	BG928008 HNC45-1-H
43	5.1	22	8	AZ320488	AZ320488 IM0040M01
44	5.1	22	8	AZ394940	AZ394940 IM0466B15
45	5.1	22	8	AZ626143	AZ626143 T. brucei
46	5.1	23	8	TA88A08P	TA88A08P T. brucei
47	5.1	23	8	AZ309024	AZ309024 IM0012H07
48	5.1	26	8	AG203256	AG203256 Pan. trogl
49	5.1	26	8	AZ393417	AZ393417 IM0156A01
50	5.1	28	8	AZ789510	AZ789510 2M0037B24
51	5.1	29	8	AG199618	AG199618 Pan. trogl
52	5.1	29	8	AJ655586	AJ655586 AJ655586
53	5.1	30	1	AZ328130	AZ328130 IM0051D16
54	5.1	30	8	CG724260	CG724260 111908D00
55	5.1	32	1	AJ666515	AJ666515 AJ666515
56	5.1	32	8	AQ025394	AQ025394 EP(X)1148
57	5.1	32	8	AZ666461	AZ666461 IM0548C09
58	5.1	33	8	AZ799336	AZ799336 2M0056E08
59	5.1	33	8	CD029243	CD029243 mgns010xK
60	5.1	34	8	BZ597035	BZ597035 SALK 0992
61	5.1	34	9	DM545957	DM545957 Drosophila
62	5.1	34	9	TA286G02P	TA286G02P T. brucei
63	5.1	34	9	AV832693	AV832693 AV832693
64	5.1	35	6	CD529971	CD529971 04N06 Atr
65	5.1	35	6	AJ664996	AJ664996 AJ664996
66	5.1	37	1	AZ310302	AZ310302 IM0025P09
67	5.1	37	8	AG194062	AG194062 Pan. trogl
68	5.1	37	8	BF137365	BF137365 601780736
69	5.1	38	2	AL941966	AL941966 Arabidops
70	5.1	38	9	AZ474228	AZ474228 IM0290G07
71	5.1	39	8	CC798073	CC798073 SALK 1457
72	5.1	39	9	CL983153	CL983153 GC0392 TI
73	5.1	40	1	AA937425	AA937425 o109b08.s
74	5.1	40	1	AU259419	AU259419 AU259419
75	5.1	40	4	BJ036081	BJ036081 AU259419
76	5.1	40	8	AZ457924	AZ457924 IM0261F04
77	5.1	40	9	CC799927	CC799927 01S0783-0
78	5.1	40	9	CL439554	CL439554 PST9498-N
79	5.1	41	9	BH625409	BH625409 1007107B1
80	5.1	41	9	CG716757	CG716757 1119046B1
81	5.1	42	8	AZ623083	AZ623083 IM0460C24
82	5.1	43	1	AA838558	AA838558 oca39d09.s
83	5.1	43	8	BH847687	BH847687 SALK 0558
84	5.1	43	8	AG228820	AG228820 Lotus cor
85	5.1	43	9	CL528342	CL528342 ASV258A08
86	5.1	44	8	AZ453388	AZ453388 IM0252A13
87	5.1	44	8	AZ873907	AZ873907 2M0187A20
88	5.1	44	8	BH905113	BH905113 SALK 1056
89	5.1	44	8	CL234280	CL234280 02S0288-0
90	5.1	45	9	TA44E02P	TA44E02P Arabidops
91	5.1	45	9	AG215464	AG215464 Drosophila
92	5.1	46	4	BG320864	BG320864 Zm04.09C0
93	5.1	46	4	BH636244	BH636244 1008010A0
94	5.1	46	8	BH902367	BH902367 SALK 0917
95	5.1	46	8	CC455214	CC455214 SALK 0665
96	5.1	46	8	CR398952	CR398952 Arabidops
97	5.1	46	9		

c 98 11 5.1 46 9 CG717980 1119051B0
c 99 11 5.1 47 1 AJ790024 AJ790024
100 11 5.1 47 8 AZ587600 AZ587600 1M0395F23

ALIGNMENTS

RESULT 1

BE373472 43 bp mRNA linear EST 21-JUL-2000
LOCUS 601225642F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3584194 5',
DEFINITION mRNA sequence.

ACCESSION

BE373472

VERSION

BE373472.1 GI:9318835

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 43)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
Plate: LAM8742 row: c column: 11
High quality sequence stop: 43.
Location/Qualifiers

FEATURES

source

1. 43

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:3584194"

/tissue_type="tumor, biopsy sample"

/dev_stage="3 months, virgin"

/lab_host="MDH10B"

/clone_lib="NCI_CGAP_Mam1"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 6.5%; Score 14; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 GACCTCCCAACGG 151

Db 9 GACCTCCCAACGG 22

RESULT 2

AUI06554

LOCUS 50 bp mRNA linear EST 28-JAN-2004

DEFINITION AUI06554 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

KA705773, mRNA sequence.

ACCESSION AUI06554

VERSION AUI06554.1 GI:13556075

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 50)

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A., and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

MEDLINE

11375929

PUBMED

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuk@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A., and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KAT05773"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 6.5%; Score 14; DB 1; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GCCGGCCACAGTTC 16

Db 12 GCCGGCCACAGTTC 25

RESULT 3

AZ841487

LOCUS 30 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0139C01R Mouse 10kb plasmid UGCM library Mus musculus genomic

clone UGCM0139C01 R, genomic survey sequence.

ACCESSION AZ841487

VERSION AZ841487.1 GI:13011395

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Place: 0139 row: C column: 01

Seq primer: CACACAGAAACAGCTATACAC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1. 30

/organism="Mus musculus"

/mol_type="genomic DNA"

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 226.089 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-10

Perfect score: 215
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

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4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
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11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	7.0	45	3	AA69465 Synthetic
C 2	15	7.0	45	6	ABL35708 TWP-TWP g
C 3	15	7.0	50	6	ABZ07185 Human leu
4	14	6.5	17	10	ADD20923 Human GAP
5	14	6.5	17	10	ADD20926 Human GAP
6	14	6.5	17	10	ADD20924 Human GAP
7	14	6.5	17	10	ADD20925 Human GAP
8	14	6.5	25	9	AC159420 Human mic
C 9	10	6.5	25	10	ADD01408 Human TCH
10	14	6.5	25	10	ADD21221 Human GAP
11	14	6.5	25	10	ADD21215 Human GAP
12	14	6.5	25	10	ADD21216 Human GAP
13	14	6.5	25	10	ADD21222 Human GAP
14	14	6.5	25	10	ADD21211 Human GAP
15	14	6.5	25	10	ADD21220 Human GAP
16	14	6.5	25	10	ADD21212 Human GAP
17	14	6.5	25	10	ADD21214 Human GAP
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19	14	6.5	25	10	ADD21218 Human GAP
20	14	6.5	25	10	ADD21217 Human GAP

21	14	6.5	25	10	ADD21213	ADD21213 Human GAP
C 22	14	6.5	25	12	ADP17305	ADP17305 Renal cel
23	14	6.5	39	5	AC83903	AC83903 PCR prime
24	14	6.5	41	5	AC83902	AC83902 PCR prime
25	14	6.5	41	5	AC83906	AC83906 PCR prime
26	14	6.5	41	5	AC83901	AC83901 PCR prime
27	14	6.5	41	5	AC83900	AC83900 PCR prime
28	14	6.5	41	5	AC83907	AC83907 PCR prime
29	14	6.5	41	5	AC83910	AC83910 PCR prime
30	14	6.5	41	5	AC83909	AC83909 PCR prime
31	14	6.5	44	5	AD20735	AD20735 Human PH1
32	14	6.5	44	5	AC83896	AC83896 PCR prime
33	14	6.5	44	5	AC83904	AC83904 PCR prime
34	14	6.5	44	5	AC83905	AC83905 PCR prime
35	14	6.5	44	5	AC83894	AC83894 PCR prime
36	14	6.5	44	5	AC83895	AC83895 PCR prime
37	14	6.5	44	5	AC83908	AC83908 PCR prime
38	14	6.5	44	5	AC83897	AC83897 PCR prime
39	14	6.5	44	5	AC83898	AC83898 PCR prime
40	14	6.5	44	5	AC83899	AC83899 PCR prime
41	14	6.5	44	10	ABX79090	ABX79090 Mucin 1 (
42	14	6.5	48	6	ABK24115	ABK24115 laminin p
C 43	14	6.5	50	4	AA176799	AA176799 Human sll
C 44	13	6.0	15	6	ABL45847	ABL45847 Human EDG
45	13	6.0	17	2	AAV96402	AAV96402 Potato ci
46	13	6.0	17	2	AAV96403	AAV96403 Potato ci
C 47	13	6.0	17	2	AAV99312	AAV99312 C. elegans
48	13	6.0	17	10	ADB40744	ADB40744 Tumour su
49	13	6.0	17	10	ADD20922	ADD20922 Human GAP
50	13	6.0	17	10	ADD20927	ADD20927 Human GAP
C 51	13	6.0	18	2	AAZ21791	AAZ21791 Exemplary
C 52	13	6.0	18	6	ABT05110	ABT05110 TNFRI exp
C 53	13	6.0	18	13	ADP06140	ADP06140 Human TNF
C 54	13	6.0	19	2	AAQ92486	AAQ92486 Cytochrome
55	13	6.0	19	2	AAZ26850	AAZ26850 Human chr
56	13	6.0	19	2	AAZ26849	AAZ26849 Human chr
57	13	6.0	19	10	ADG34897	ADG34897 Human TNF
C 58	13	6.0	19	10	ADG35020	ADG35020 Human TNF
59	13	6.0	20	2	AAV09923	AAV09923 Fusarium
60	13	6.0	20	12	ADH68616	ADH68616 Rosa sp f
C 61	13	6.0	21	4	AAF82345	AAF82345 Murine in
C 62	13	6.0	21	6	ABO81614	ABO81614 INOS rela
C 63	13	6.0	21	10	ACF79346	ACF79346 Phenylala
64	13	6.0	21	12	ADK95295	ADK95295 Primer of
C 65	13	6.0	23	12	ADN35332	ADN35332 Human NSC
C 66	13	6.0	23	12	ADN48538	ADN48538 PCR prime
C 67	13	6.0	24	3	ABK10968	ABK10968 PCR prime
68	13	6.0	24	6	AB182804	AB182804 Capture o
69	13	6.0	24	6	AB192070	AB192070 Capture o
C 70	13	6.0	24	6	AB192071	AB192071 Capture o
C 71	13	6.0	25	6	AB182805	AB182805 Capture o
C 72	13	6.0	25	6	ABK86313	ABK86313 Mouse TGR
73	13	6.0	25	9	ACHS9338	ACHS9338 DNA large
74	13	6.0	25	10	ADD21223	ADD21223 Human GAP
C 75	13	6.0	25	10	ADD21210	ADD21210 Human GAP
76	13	6.0	29	10	ADK71528	ADK71528 Drug-tole
C 77	13	6.0	31	6	ABK21680	ABK21680 Human ERG
C 78	13	6.0	31	8	ABZ64249	ABZ64249 Human H-R
C 79	13	6.0	31	8	ABZ66128	ABZ66128 Human HER
C 80	13	6.0	31	8	ACD61854	ACD61854 HCV minus
C 81	13	6.0	31	12	AD190049	AD190049 HCV DNAzy
C 82	13	6.0	33	6	ABA04974	ABA04974 Ribosomal
83	13	6.0	35	10	ADL07530	ADL07530 F. pastor
84	13	6.0	39	10	ABZ26067	ABZ26067 EHV BAC r
85	13	6.0	39	12	ADH70031	ADH70031 Human Vbe
C 86	13	6.0	39	12	ADL64622	ADL64622 Human sdn
C 87	13	6.0	40	3	ADQ36616	ADQ36616 Exophiala
88	13	6.0	40	3	AAA51111	AAA51111 Oligomer
C 89	13	6.0	40	6	AAAS1142	AAAS1142 Oligomer
90	13	6.0	40	6	ABK69697	ABK69697 Human WTL
91	13	6.0	40	8	ACA93369	ACA93369 Recombina
92	13	6.0	40	10	ADB67573	ADB67573 Human WT-
93	13	6.0	40	10	ADJ80806	ADJ80806 Wilms tu

94	13	6.0	40	12	ADJ83726	Oligonucleotide
95	13	6.0	40	12	ADJ57614	Human WT
96	13	6.0	40	12	ADJ09169	Human WT
97	13	6.0	42	2	AAQ23424	Probe for
98	13	6.0	42	2	AAQ44162	Probe for
99	13	6.0	42	2	AAQ37218	inse
100	13	6.0	42	2	AAV12516	Probe for

ALIGNMENTS

RESULT 1

AAA69465/c
ID AAA69465 standard; DNA; 45 BP.

AAA69465;

31-OCT-2000 (first entry)

Synthetic TMP-Fc gene construction oligonucleotide SEQ ID NO:379.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF;
immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase; asthma;
thrombosis; pharmaceutical; PCR primer; ss.

Homo sapiens.
Synthetic.

WO200024782-A2.

04-MAY-2000.

25-OCT-1999; 99WO-US025044.

23-OCT-1998; 98US-0105371P.

22-OCT-1999; 99US-00428082.

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.

Example 2; Page 329; 608pp; English.

The present invention describes composition of matter (1) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (1) is: (X1)-a-P1-(X2)-b, where: P1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antineoplastic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention

Sequence 45 BP; 9 A; 11 C; 17 G; 8 T; 0 U; 0 Other;

Query Match	7.0%	Score 15;	DB 3;	Length 45;
Best Local Similarity	100.0%	Pred. No. 8.2e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

116 CACGCGCTCCACACAG 130
|||
28 CACGCGCTCCACACAG 14

RESULT 2

ABL35708/c
ID ABL35708 standard; DNA; 45 BP.

ABL35708;

05-APR-2002 (first entry)

TMP-Fc gene construction oligonucleotide SEQ ID NO:379.

Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
TPO mimetic peptide; EPO mimetic peptide; EGF; VEGF antagonist;
MMP inhibitor; antiinflammatory; antitumor; immunosuppressive;
cytostatic; antineoplastic; antiarthritic; antidiabetic; ophthalmological;
antineoplastic; anorectic; antiferility; haemostatic; dermatological;
neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
sleep disorder; neurological degenerative disease; anaemia;
chromocytoma; metastatic tumour; systemic lupus erythematosus;
Fanconi's syndrome; PCR primer; ss.

Homo sapiens.
Synthetic.

WO200183525-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US014310.

03-MAY-2000; 2000US-00563286.

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham JC, Boone TC, Gudas JW;

WPI; 2002-130313/17.

Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.

Example 2; Page 103; 176pp; English.

The present invention describes a vehicle-peptide molecule (1) or its multimers. (1) can have antineoplastic, antitumor, immunosuppressive, cytostatic, antineoplastic, antiarthritic, antidiabetic, ophthalmological and neuroprotective activities. (1) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (1) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (1) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, cancer, infertility, and neurological degenerative diseases. (1), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 : Search time 222.638 Seconds
(without alignments)
4536.068 Million cell updates/sec

Title: US-09-887-941B-9

Perfect score: 145
Sequence: 1 tggagcagcagcattccctccct.....nnaagttgagctctccc 145

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 844130 seqs, 3482420727 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Published Applications_NA.*

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21: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	11.7	25	US-10-719-900-170745	Sequence 170745, Ap
2	17	11.7	25	US-10-809-189-5883	Sequence 5883, Ap
3	17	11.7	25	US-10-719-956-524224	Sequence 524224, A
4	16	11.0	25	US-10-809-189-122026	Sequence 122026, A
5	16	11.0	25	US-10-956-157-201846	Sequence 201846, A
6	16	11.0	25	US-10-956-157-247188	Sequence 247188, A
7	16	11.0	25	US-10-956-157-253662	Sequence 253662, A

8	16	11.0	25	US-11-036-317-94502	Sequence 94502, A
9	16	11.0	25	US-11-036-317-95477	Sequence 95477, A
10	15	10.3	17	US-09-848-754A-445	Sequence 445, App
11	15	10.3	17	US-09-848-754A-1750	Sequence 1750, Ap
12	15	10.3	22	US-10-845-057-143	Sequence 143, App
13	15	10.3	22	US-10-845-057-449	Sequence 449, App
14	15	10.3	25	US-10-719-900-108447	Sequence 108447, A
15	15	10.3	25	US-10-719-900-409239	Sequence 409239, A
16	15	10.3	25	US-10-809-189-38929	Sequence 38929, A
17	15	10.3	25	US-10-956-157-304970	Sequence 304970, A
18	15	10.3	25	US-10-719-956-3771	Sequence 3771, Ap
19	15	10.3	24	US-11-036-317-567671	Sequence 567671, A
20	15	10.3	17	US-09-848-754A-1749	Sequence 1749, Ap
21	14	9.7	17	US-10-363-177A-43	Sequence 43, App1
22	14	9.7	16	US-10-251-117-766	Sequence 766, App
23	14	9.7	19	US-10-251-117-1073	Sequence 1073, App
24	14	9.7	22	US-10-923-354-712	Sequence 712, App
25	14	9.7	19	US-10-923-354-1019	Sequence 1019, App
26	14	9.7	21	US-10-751-736-29063	Sequence 29063, A
27	14	9.7	21	US-10-751-736-32216	Sequence 32216, A
28	14	9.7	25	US-10-098-263B-84817	Sequence 84817, A
29	14	9.7	25	US-10-719-900-185005	Sequence 185005, A
30	14	9.7	25	US-10-719-900-246219	Sequence 246219, A
31	14	9.7	25	US-10-719-900-249184	Sequence 249184, A
32	14	9.7	25	US-10-719-900-260808	Sequence 260808, A
33	14	9.7	25	US-10-719-900-327252	Sequence 327252, A
34	14	9.7	25	US-10-719-900-335121	Sequence 335121, A
35	14	9.7	25	US-10-719-900-354142	Sequence 354142, A
36	14	9.7	25	US-10-719-900-534440	Sequence 534440, A
37	14	9.7	25	US-10-719-900-539535	Sequence 539535, A
38	14	9.7	25	US-10-719-900-642806	Sequence 642806, A
39	14	9.7	25	US-10-719-900-798504	Sequence 798504, A
40	14	9.7	25	US-10-719-900-824514	Sequence 824514, A
41	14	9.7	25	US-10-719-900-973647	Sequence 973647, A
42	14	9.7	25	US-10-809-189-7934	Sequence 7934, App
43	14	9.7	25	US-10-809-189-7945	Sequence 7945, App
44	14	9.7	25	US-10-809-189-7946	Sequence 7946, App
45	14	9.7	25	US-10-809-189-7947	Sequence 7947, App
46	14	9.7	25	US-10-956-157-84715	Sequence 84715, A
47	14	9.7	25	US-10-956-157-84716	Sequence 84716, A
48	14	9.7	25	US-10-956-157-84717	Sequence 84717, A
49	14	9.7	25	US-10-956-157-84718	Sequence 84718, A
50	14	9.7	25	US-10-956-157-84719	Sequence 84719, A
51	14	9.7	25	US-10-956-157-84720	Sequence 84720, A
52	14	9.7	25	US-10-956-157-84721	Sequence 84721, A
53	14	9.7	25	US-10-956-157-84722	Sequence 84722, A
54	14	9.7	25	US-10-956-157-84723	Sequence 84723, A
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56	14	9.7	25	US-10-956-157-84725	Sequence 84725, A
57	14	9.7	25	US-10-956-157-84726	Sequence 84726, A
58	14	9.7	25	US-10-956-157-84727	Sequence 84727, A
59	14	9.7	25	US-10-956-157-84728	Sequence 84728, A
60	14	9.7	25	US-10-956-157-84729	Sequence 84729, A
61	14	9.7	25	US-10-956-157-84730	Sequence 84730, A
62	14	9.7	25	US-10-956-157-84731	Sequence 84731, A
63	14	9.7	25	US-10-956-157-84732	Sequence 84732, A
64	14	9.7	25	US-10-956-157-84733	Sequence 84733, A
65	14	9.7	25	US-10-956-157-84734	Sequence 84734, A
66	14	9.7	25	US-10-956-157-84735	Sequence 84735, A
67	14	9.7	25	US-10-956-157-84736	Sequence 84736, A
68	14	9.7	25	US-10-956-157-84737	Sequence 84737, A
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79	14	9.7	25	US-10-956-157-84748	Sequence 84748, A
80	14	9.7	25	US-10-956-157-84749	Sequence 84749, A

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C 82 13 9.0 23 9 US-09-860-784-104 Sequence 104, App
C 83 13 9.0 25 15 US-10-098-263B-5398 Sequence 5398, Ap
C 84 13 9.0 25 15 US-10-098-263B-50326 Sequence 90326, A
C 85 13 9.0 25 21 US-10-719-900-7096 Sequence 7096, Ap
C 86 13 9.0 25 21 US-10-719-900-35838 Sequence 35838, A
C 87 13 9.0 25 21 US-10-719-900-59789 Sequence 59789, A
C 88 13 9.0 25 21 US-10-719-900-106507 Sequence 106507,
C 89 13 9.0 25 21 US-10-719-900-109506 Sequence 109506,
C 90 13 9.0 25 21 US-10-719-900-112867 Sequence 112867,
C 91 13 9.0 25 21 US-10-719-900-113381 Sequence 113381,
C 92 13 9.0 25 21 US-10-719-900-171200 Sequence 171200,
C 93 13 9.0 25 21 US-10-719-900-178551 Sequence 178551,
C 94 13 9.0 25 21 US-10-719-900-224055 Sequence 224055,
C 95 13 9.0 25 21 US-10-719-900-268928 Sequence 268928,
C 96 13 9.0 25 21 US-10-719-900-292775 Sequence 292775,
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C 100 13 9.0 25 21 US-10-719-900-505181 Sequence 505181,
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ALIGNMENTS

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RESULT 1
US-10-719-900-170745
; Sequence 170745, Application US/107199900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-170745
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Query Match 11.7%; Score 17; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 84 CCAAAAATTCAGCTC 100
Db 3 CCAAAAATTCAGCTC 19
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RESULT 2
US-10-809-189-5883
; Sequence 5883, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-5883
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Query Match 11.7%; Score 17; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 84 CCAAAAATTCAGCTC 100
Db 6 CCAAAAATTCAGCTC 22
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RESULT 3
US-10-719-956-524224
; Sequence 524224, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 524224
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-524224
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 84 CCAAAAATTCAGCTC 100
Db 7 CCAAAAATTCAGCTC 23
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RESULT 4
US-10-809-189-122026
; Sequence 122026, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-122026
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Query Match 11.0%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 ; Search time 44.4954 Seconds
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Title: US-09-887-941b-9

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Scoring table: OLIGO NUC
Gapex 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	15	10.3	17	4	US-09-401-063-445
6	15	10.3	25	4	US-09-396-196G-38929
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ALIGNMENTS

RESULT 1
US-09-396-196G-5883

; Sequence 5883, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affimetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5883

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; US-09-396-196G-5883

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Best Local Similarity 100.0%; Pred. No. 17;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-238-972-12/C

; Sequence 12, Application US/09238972

; Patent No. 6784163

; GENERAL INFORMATION:

; APPLICANT: MacLeod, Carol L.

; TITLE OF INVENTION: Inhibition of Cationic Amino Acid Transporter Protein

; TITLE OF INVENTION: and Uses Thereof

; FILE REFERENCE: D5232CTP3

; CURRENT APPLICATION NUMBER: US/09/238,972

; CURRENT FILING DATE: 1999-01-27

; EARLIER APPLICATION NUMBER: US 08/187,634

; EARLIER FILING DATE: 1994-26-01

; NUMBER OF SEQ ID NOS: 16

; SEQ ID NO 12

; LENGTH: 25

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: primer bind

; OTHER INFORMATION: Primer used to clone the NOS2 cDNA by RT/PCR

; OTHER INFORMATION: from mouse mammary tumor cDNA

; US-09-238-972-12

Query Match 11.0%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 60;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||DB 25 TTCAGCTCAAGACC 10
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RESULT 3

US-09-396-196G-122026

; Sequence 122026, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affimetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 122026

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

; US-09-396-196G-122026

Query Match 11.0%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 60;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-08-985-162-445

; Sequence 445, Application US/08985162

; Patent No. 6057156

; GENERAL INFORMATION:

; APPLICANT: Akhtar, Saghir

; APPLICANT: McSwigen, James

; APPLICANT: Fell, Patricia

; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT

; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED

; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH

; TITLE OF INVENTION: FACTOR RECEPTORS

; NUMBER OF SEQUENCES: 1877

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,162

; FILING DATE: 04 December 1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/036,476

; FILING DATE: 31 January 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Marburg, Richard J.

; REGISTRATION NUMBER: 32,337

; REFERENCE/DOCKET NUMBER: 230/107

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 445:

; SEQUENCE CHARACTERISTICS:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 1008.54 Seconds
(without alignments)
5472.564 Million cell updates/sec

Title: US-09-887-941B-9

Perfect score: 145

Sequence: 1 tGagagcagcatctctccct.....maaaagttcagctctcc 145

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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TA157G06P	T. brucei
TA211D06P	T. brucei
TA240H09P	T. brucei
AZ321671	1M0402017
TA157B05P	T. brucei
TA356B09P	T. brucei
AJ668296	AJ668296
BX563569	BX563569
CF335916	JMT--05-M
AZ469660	1M0283J13
AZ795776	2M0051K11
AI149305	qC72d06.x
AI471126	tf90e05.x
AI471696	tf99f05.x
AI587718	AL587718
AU256661	AU256661
AZ664439	1M0544A07

98 11 7.6 25 8 AZ804762
 C 99 11 7.6 25 8 AZ830405
 C 100 11 7.6 25 8 AZ855418 AZ855418 2M0159M21

ALIGNMENTS

RESULT 1
 BG720096/c 44 bp mRNA linear EST 08-MAY-2001

DEFINITION 602691016F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4823642 5',
 mRNA sequence.

ACCESSION BG720096
 VERSION BG720096.1 GI:13999283
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC Http://mgs.nci.nih.gov/
 1 (bases 1 to 44)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

EMAIL: cgabbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LHAM10733 row: 0 column: 03
 High quality sequence stop: 44.

Location/Qualifiers
 1..44

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4823642"

/lab_host="DH10B"

/clone_1lb="NIH MGC 97"

/note="Organ: testis; Vector: pBluescript (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTVA-3', size-selected for average

insert size 2.2 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Query Match 11.0%; Score 16; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 CCGCGGCCCCCAAAA 90
 Db 33 CCGCGGCCCCCAAAA 18

RESULT 2
 AZ479867/c 39 bp DNA linear GSS 04-OCT-2000

LOCUS AZ479867
 DEFINITION 1M0300H24R Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0300H24 R, genomic survey sequence.

ACCESSION AZ479867.1 GI:10640881
 VERSION AZ479867.1
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 39)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0300 row: H column: 24
 Seq primer: CACACAGAAACGCTATGACC
 class: plasmid ends
 High quality sequence stop: 39.

Location/Qualifiers
 1..39

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0300H24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1lb="Mouse 10kb plasmid UUC1M library"

/note="Vector: pMD22v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (GI:473211419b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 10.3%; Score 15; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 GGGCCCCCAAAAAT 92
 Db 15 GGGCCCCCAAAAAT 1

RESULT 3
 TA21H040 30 bp DNA linear GSS 13-DEC-2000

LOCUS TA21H040
 DEFINITION T. Brucei sheared genomic DNA clone 21h04, reverse sequence,

genomic survey sequence.

ACCESSION TA21H040
 VERSION TA21H040.1 GI:11844162
 KEYWORDS GSS.


```
c 94      12      8.3      13      5      ABH28500      Abh28500 Oligonuc1
95      12      8.3      13      5      ABR65357      ABR65357 Oligonuc1
96      12      8.3      13      5      ABC69097      ABC69097 Oligonuc1
c 97      12      8.3      14      2      AAV57033      AAV57033 Human Not
c 98      12      8.3      14      12      ADO80078      ADO80078 Human alp
c 99      12      8.3      15      3      AAs53258      AAs53258 Aryl hydr
c 100     12      8.3      16      3      AAs95719      AAs95719 Oligonuc1
```

ALIGNMENTS

RESULT 1

```
AAA74753/C
ID AAA74753 standard; cDNA; 25 BP.
```

```
AC AAA74753;
```

```
DT 08-JAN-2001 (first entry)
```

```
XX Mouse mammary tumour NOS2 cDNA primer #2.
```

```
XX Mouse; cationic amino acid transporter protein; CAT2 transporter;
KW antibacterial; immunosuppressive; cytosolic; dermatological;
KW antiinflammatory; antirheumatic; antidiabetic; neuroprotective;
KW immunomodulator; cardiac; cerebroprotective; protozoicide; sepsis;
KW breast cancer; lung cancer; autoimmune disease; cachexia;
KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW cerebral malaria; cardiovascular disease; capillary leak syndrome; ss.
```

```
XX Mus sp.
```

```
XX WO200044766-A1.
```

```
XX 03-AUG-2000.
```

```
XX 27-JAN-2000; 2000WO-US002041.
```

```
XX 27-JAN-1999; 99US-00238972.
```

```
XX (RERE-) RES DEV FOUND.
```

```
XX Macleod CL;
```

```
XX MPI; 2000-491236/43.
```

```
XX Inhibiting cationic amino acid transport by using an antisense
PT oligonucleotide directed against CAT2 mRNA, useful for treating sepsis,
PT neoplastic disease (e.g. breast cancer) and autoimmune diseases (e.g.
PT rheumatoid arthritis).
```

```
XX Example 25; Page 48; 94pp; English.
```

```
XX The present sequence is a primer which was used to clone the NOS2 cDNA
CC probe by RT-PCR from mouse mammary tumour cDNA. This was part of an
CC example to demonstrate the use of an antisense oligonucleotide directed
CC against CAT2 mRNA to inhibit cationic amino acid transport. Cat2 is one
CC of three genes encoding a transport system which mediates the majority of
CC arginine transport in most cells and tissues. Arginine and its transport
CC are essential for the regulated production of nitric oxide. The method is
CC therefore useful for inhibiting the production of nitric oxide. It is
CC also useful for treating a pathophysiological state characterised by
CC production of an undetectable level of nitric oxide. Such conditions
CC include sepsis, neoplastic disease (e.g. breast cancer or lung cancer),
CC autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid
CC arthritis or multiple sclerosis), cachexia, cerebral malaria,
CC cardiovascular disease, cerebrovascular disease or capillary leak
CC syndrome
```

```
XX Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
```

```
Query Match 11.0%; Score 16; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
```

```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 92 TTCCAGCTCAAGACC 107
```

```
DB 25 TTCCAGCTCAAGACC 10
```

RESULT 2

```
AAV97665
ID AAV97665 standard; RNA; 17 BP.
```

```
AC AAV97665;
```

```
DT 17-MAR-1999 (first entry)
```

```
XX Human EGF-R target sequence nucleotide position 3843.
```

```
XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW cancer; genetic drift; detection; mutation; ss.
```

```
XX Homo sapiens.
```

```
XX MO9833893-A2.
```

```
XX 06-AUG-1998.
```

```
XX 14-JAN-1998; 98MO-US000730.
```

```
XX 31-JAN-1997; 97US-0036476P.
```

```
XX 04-DEC-1997; 97US-00985162.
```

```
XX (RIBO-) RIBOZYME PHARM INC.
```

```
XX (UNAS-) UNIV ASTON.
```

```
XX Akhtar S, Fell P, Mcswiggen JA;
```

```
XX MPI; 1998-437449/37.
```

```
XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and for
PT treating cancers.
```

```
XX Claim 5; Page 77; 109pp; English.
```

```
XX The present invention describes enzymatic nucleic acid molecules (NMs)
CC which specifically cleave RNA derived from an epidermal growth factor
CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC represent specifically claimed target sequence from human EGF-R. AAV98044
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC hairpin ribozymes respectively for human EGF-R. The NMs are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NMs can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell
```

```
XX Sequence 17 BP; 7 A; 5 C; 2 G; 0 T; 3 U; 0 Other;
```

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Query Match 10.3%; Score 15; DB 2; Length 17;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
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```
OY 103 GAGCCCTAAATTC 117
```

```
DB 2 GAGCCCTAAATTC 16
```

RESULT 3

```
ABN79943
ID ABN79943 standard; DNA; 17 BP.
```

```
AC ABN79943;
```

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 889.692 Seconds
(without alignments)
7897.122 Million cell updates/sec

Title: US-09-887-941B-9
Perfect score: 145
Sequence: 1 tgagagacagcatcctccccc.....mnaagtttgagcttccccc 145

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

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1: gb_ba:*
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9: gb_pri:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	10.3	17	6	AR402105 Sequence
2	15	10.3	17	6	BD067605 Enzymatic
3	15	10.3	21	9	AF480506 Homo sapi
4	15	10.3	21	9	HSAS50402 Homo sapi
5	15	10.3	21	9	HSAS50403 Homo sapi
6	14	9.7	17	6	AX398166 Sequence
7	14	9.7	17	6	AX739187 Sequence
8	14	9.7	20	6	BD177288 Sulforan
9	14	9.7	30	6	AX793166 Sequence
10	14	9.7	46	6	BD093895 A method
11	14	9.7	50	6	BD093895 A method
12	14	9.7	50	6	BD093895 A method
13	14	9.7	50	6	BD093895 A method
14	14	9.7	50	6	BD093895 A method
15	14	9.7	50	6	BD093895 A method
16	14	9.7	50	6	BD093895 A method
17	14	9.7	50	6	BD093895 A method
18	14	9.7	50	6	BD093895 A method
19	14	9.7	50	6	BD093895 A method

C 20	13	9.0	20	6	AR066926 Sequence
C 21	13	9.0	20	6	AX127891 Sequence
C 22	13	9.0	20	6	AX139878 Sequence
C 23	13	9.0	24	6	AX643171 Sequence
C 24	13	9.0	27	6	A07481 Nucleotide
C 25	13	9.0	27	6	A07483 Nucleotide
C 26	13	9.0	27	6	A07485 Nucleotide
C 27	13	9.0	27	6	AR308673 Sequence
C 28	13	9.0	31	6	AX249028 Sequence
C 29	13	9.0	33	6	AR123937 Sequence
C 30	13	9.0	33	6	AR123938 Sequence
C 31	13	9.0	40	9	HUMDB09M3
C 32	13	9.0	41	6	AR263968 Sequence
C 33	13	9.0	47	6	AX522757 Sequence
C 34	13	9.0	47	6	BD013381 Novel pro
C 35	13	9.0	47	6	BD013388 Novel pro
C 36	13	9.0	48	6	A07498 Nucleotide
C 37	13	9.0	48	6	A07500 Nucleotide
C 38	13	9.0	48	6	A07502 Nucleotide
C 39	13	9.0	50	6	AR032829 Sequence
C 40	13	9.0	50	6	129569 Sequence 44
C 41	13	9.0	50	6	191243 Sequence 44
C 42	13	9.0	50	6	AR209493 Sequence
C 43	13	9.0	50	6	BD013694 Method of
C 44	13	9.0	14	6	AR300232 Sequence
C 45	12	8.3	15	6	AR128944 Sequence
C 46	12	8.3	17	6	BD258400 Regulator
C 47	12	8.3	17	6	AX649106 Sequence
C 48	12	8.3	17	6	AX649107 Sequence
C 49	12	8.3	17	6	AX649108 Sequence
C 50	12	8.3	17	6	AX649109 Sequence
C 51	12	8.3	17	6	AX649110 Sequence
C 52	12	8.3	17	6	AX649111 Sequence
C 53	12	8.3	17	6	AX757975 Sequence
C 54	12	8.3	18	6	A14818 Nucleotide
C 55	12	8.3	18	6	CQ876365 Sequence
C 56	12	8.3	19	6	AR292449 Sequence
C 57	12	8.3	20	6	AR049901 Sequence
C 58	12	8.3	20	6	BD183569 Method fo
C 59	12	8.3	20	6	BD266805 Sequence
C 60	12	8.3	20	6	CQ785772 Sequence
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C 62	12	8.3	21	6	AR298353 Sequence
C 63	12	8.3	21	6	AX088797 Sequence
C 64	12	8.3	21	6	AX297605 Sequence
C 65	12	8.3	22	6	AR107513 Sequence
C 66	12	8.3	22	6	AR158132 Sequence
C 67	12	8.3	22	6	AR158132 Sequence
C 68	12	8.3	22	6	BD137791 Protein e
C 69	12	8.3	22	6	184203 Sequence 1
C 70	12	8.3	22	6	AR274473 Sequence
C 71	12	8.3	22	6	AR353117 Sequence
C 72	12	8.3	22	6	AR493411 Sequence
C 73	12	8.3	22	6	AX815754 Sequence
C 74	12	8.3	23	6	CQ878634 Sequence
C 75	12	8.3	23	6	AX148278 Sequence
C 76	12	8.3	23	6	AX921611 Sequence
C 77	12	8.3	23	6	AX921623 Sequence
C 78	12	8.3	23	6	BD063890 Nucleic a
C 79	12	8.3	24	6	AR180830 Sequence
C 80	12	8.3	24	6	AR349788 Sequence
C 81	12	8.3	24	6	AX291132 Sequence
C 82	12	8.3	24	6	AX454948 Sequence
C 83	12	8.3	24	6	AX488599 Sequence
C 84	12	8.3	25	6	AR038302 Sequence
C 85	12	8.3	25	6	158591 Sequence 13
C 86	12	8.3	25	6	AX088796 Sequence
C 87	12	8.3	25	6	AX650610 Sequence
C 88	12	8.3	25	6	AX650611 Sequence
C 89	12	8.3	25	6	AX650612 Sequence
C 90	12	8.3	25	6	AX650613 Sequence
C 91	12	8.3	25	6	AX650614 Sequence
C 92	12	8.3	25	6	AX650615 Sequence

93 12 8.3 25 6 AX650616 Sequence
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 95 12 8.3 25 6 AX650618 Sequence
 96 12 8.3 25 6 AX650619 Sequence
 97 12 8.3 25 6 AX650620 Sequence
 98 12 8.3 25 6 AX650621 Sequence
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 100 12 8.3 25 6 AX650623 Sequence

ALIGNMENTS

RESULT 1
 LOCUS AR402105 17 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 445 from patent US 6623962.
 ACCESSION AR402105
 VERSION AR402105.1 GI:40149555
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 AUTHORS 1 (bases 1 to 17)
 TITLE Akhtar,S., Fell,P. and McSwiggen,J.A.
 JOURNAL Enzymatic nucleic acid treatment of diseases or conditions related
 to levels of epidermal growth factor receptors
 FEATURES
 source Patent: US 6623962-A 445 23-SEP-2003;
 Location/Qualifiers
 1..17
 /organism="unknown"
 /mol_type="genomic DNA"

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 Query Match 10.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAGCCCTAAATCC 117
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 2 GAGCCCTAAATCC 16

RESULT 2
 LOCUS BD067605 17 bp RNA linear PAT 27-AUG-2002
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
 to levels of epidermal growth factor receptors.
 ACCESSION BD067605
 VERSION BD067605.1 GI:22613208
 KEYWORDS JP 2001511003-A/445.
 SOURCE unidentified
 ORGANISM unidentified

COMMENT
 JOURNAL
 AUTHORS
 TITLE
 JOURNAL

REFERENCE
 1 (bases 1 to 17)
 Akhtar,S., Fell,P. and McSwiggen,J.A.
 Enzymatic nucleic acid treatment of diseases or conditions related
 to levels of epidermal growth factor receptors
 Patent: JP 2001511003-A 445 07-AUG-2001;
 RIBOZYME PHARMACEUTICALS INC,ASTON UNITV
 OS Unidentified
 PN JP 2001511003-A/445
 PD 07-AUG-2001
 PR 14-JAN-1998 JP 1998512913
 SAGRIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
 C12N9/00, C07K14/71
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC levels of epidermal growth factor receptors
 FH Key Location/Qualifiers

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 source Location/Qualifiers
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 /mol_type="genomic RNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 10.3%; Score 15; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAGCCCTAAATCC 117
 |||||
 2 GAGCCCTAAATCC 16

RESULT 3
 LOCUS AF480506 21 bp RNA linear PRI 01-MAY-2002
 DEFINITION Homo sapiens microRNA mir-108 gene, complete sequence.
 ACCESSION AF480506
 VERSION AF480506.1 GI:20378946
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS 1 (bases 1 to 21)
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 JOURNAL Mourtelatos,Z., Dostie,J., Pauskhin,S., Sharma,A., Charroux,B.,
 Abel,L., Rappsilber,J., Mann,M. and Dreyfuss,G.
 TITLE miRNPs: a novel class of ribonucleoproteins containing numerous
 microRNAs
 JOURNAL Genes Dev. 16 (6), 720-728 (2002)
 MEDLINE 21912064
 PUBMED 11914277

REFERENCE
 2 (bases 1 to 21)
 Mourtelatos,Z.

AUTHORS Direct Submission
 TITLE Submitted (05-FEB-2002) HHMI, University of Pennsylvania, CRB Room
 JOURNAL 330, 415 Curie Boulevard, Philadelphia, PA 19104-6148, USA
 LOCATION/Qualifiers

FEATURES
 source 1..21
 /organism="Homo sapiens"
 /mol_type="other RNA"
 /db_xref="taxon:9606"
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 /product="microRNA mir-108"

ORIGIN
 Query Match 10.3%; Score 15; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CCTTAAATCCTTA 120
 |||||
 16 CCTTAAATCCTTA 2

RESULT 4
 LOCUS HSA550402 21 bp RNA linear PRI 19-MAR-2003
 DEFINITION Homo sapiens microRNA mir-108-1.
 ACCESSION AJ550402
 VERSION AJ550402.1 GI:29125708
 KEYWORDS microRNA mir-108-1; mi-108-1 gene; miRNA.

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 1 Lim,L.P., Glasner,M.E., Yekta,S., Burge,C.B. and Bartel,D.P.
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 ! Search time 385.394 Seconds
(without alignments)
4536.068 Million cell updates/sec

Title: US-09-887-941B-8
Perfect score: 251
Sequence: 1 ggcggcgcttggcgacccgcgcg.....cgttcccccacgcgtgtgt 251

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 8443130 seqs, 3482420727 residues

Word size: 0

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database:

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/BCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10I_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	16	6.4	25	US-10-719-900-554749	Sequence 554749,
5	16	6.4	25	US-10-719-900-655519	Sequence 655519,
6	16	6.4	25	US-11-036-317-257707	Sequence 257707,
7	16	6.4	25	US-11-036-317-258580	Sequence 258580,

C 8	16	6.4	25	US-11-036-317-306150	Sequence 306150,
C 9	16	6.4	25	US-11-036-317-311829	Sequence 311829,
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C 14	15	6.0	25	US-10-719-900-283917	Sequence 283917,
C 15	15	6.0	25	US-10-719-900-351674	Sequence 351674,
C 16	15	6.0	25	US-10-719-900-685089	Sequence 685089,
C 17	15	6.0	25	US-10-719-900-752478	Sequence 752478,
C 18	15	6.0	25	US-10-809-189-18026	Sequence 18026, A
C 19	15	6.0	25	US-10-809-189-119467	Sequence 119467,
C 20	15	6.0	25	US-10-719-956-635767	Sequence 635767,
C 21	15	6.0	25	US-11-036-317-123125	Sequence 123125,
C 22	15	6.0	25	US-11-036-317-236859	Sequence 236859,
C 23	15	6.0	25	US-11-036-317-732922	Sequence 732922,
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C 26	14	5.6	19	US-10-922-340-146	Sequence 23, Appl
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C 57	14	5.6	25	US-10-719-956-360812	Sequence 360812,
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C 72	14	5.6	25	US-11-036-317-513211	Sequence 513211,
C 73	14	5.6	25	US-11-036-317-518814	Sequence 518814,
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C 75	14	5.6	25	US-11-036-317-771701	Sequence 771701,
C 76	14	5.6	25	US-11-036-317-775866	Sequence 775866,
C 77	14	5.6	25	US-11-036-317-803844	Sequence 803844,
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C 89 14 5.6 25 24 US-11-036-317-981000 Sequence 981000,
C 90 14 5.6 34 18 US-10-470-751-7 Sequence 7, Appl1
C 91 14 5.6 34 22 US-10-504-132-7 Sequence 384, Appl
C 92 14 5.6 15 18 US-09-993-346-384 Sequence 28, Appl
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C 95 13 5.2 17 19 US-10-138-674-2661 Sequence 2661, Ap
C 96 13 5.2 17 18 US-10-287-949A-2661 Sequence 170, App
C 97 13 5.2 18 17 US-10-388-360-170 Sequence 3004, Ap
C 98 13 5.2 18 18 US-10-138-674-3004 Sequence 3004, Ap
C 99 13 5.2 18 19 US-10-287-949A-3004 Sequence 49, Appl
C 100 13 5.2 19 15 US-10-224-005-49 Sequence 49, Appl
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ALIGNMENTS

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; Sequence 122749, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 122749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-122749
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; Sequence 183214, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 183214
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-183214
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; GENERAL INFORMATION:
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; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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US-10-719-900-422910
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; Sequence 554749, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
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US-10-719-900-554749
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
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ALIGNMENTS

RESULT 1

US-09-396-196G-18026
; Sequence 18026, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18026

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QY 196 TTGCAGTCATGAC 210
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DB 7 TTGCAGTCATGAC 21
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RESULT 2

US-09-396-196G-119467
; Sequence 119467, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-119467

Query Match

Best Local Similarity 6.0%; Score 15; DB 4; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TGCAGATGCTGTGAG 143
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DB 9 TGCAGATGCTGTGAG 23
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RESULT 3

US-08-140-349-14/C
; Sequence 14, Application US/08140349
; Patent No. 5679512

GENERAL INFORMATION:

APPLICANT: Laney, Maureen
APPLICANT: Chen, Yan
APPLICANT: Ullman, Edwin F.
APPLICANT: Hahnenberger, Karen M.
TITLE OF INVENTION: Method for Introducing Defined Sequences
TITLE OF INVENTION: at the 3' End of Polynucleotides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Behring Diagnostics Inc.
STREET: 3403 Yerba Buena Road
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95135
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,349
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,079
FILING DATE: 31-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Leitner, Theodore J.
REGISTRATION NUMBER: 28,319
REFERENCE/DOCKET NUMBER: 27660 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1091
TELEFAX: (415) 493-8870
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: synthetic
US-08-140-349-14

Query Match 6.0%; Score 15; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GGGGGGGCTTTTCTG 36
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DB 28 GGGGGGGCTTTTCTG 14
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RESULT 4

US-08-475-236-14/C
; Sequence 14, Application US/08475236
; Patent No. 5683879
; GENERAL INFORMATION:
; APPLICANT: Laney, Maureen
; APPLICANT: Chen, Yan
; APPLICANT: Ullman, Edwin F.
; APPLICANT: Hahnenberger, Karen M.
; TITLE OF INVENTION: Method for Introducing Defined Sequences
; TITLE OF INVENTION: at the 3' End of Polynucleotides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Behring Diagnostics Inc.
; STREET: 3403 Yerba Buena Road
; CITY: San Jose

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Searched: 34239544 seqs, 19032134700 residues

Word size : 0

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7: gb_est6:*
8: gb_est7:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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9	13	5.2	31	1	AA909238
10	13	5.2	34	1	AI811024
11	13	5.2	34	8	AZ346691
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16	13	5.2	50	1	BG153713
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26	12	4.8	31	1	AI431129
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36	12	4.8	40	1	AI462129
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71	11	4.4	30	8	AZ588957
72	11	4.4	31	1	AA968474
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76	11	4.4	31	1	AI917527
77	11	4.4	31	8	AZ490711
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87	11	4.4	34	8	AZ628045
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89	11	4.4	35	1	BM400381
90	11	4.4	35	8	AZ469734
91	11	4.4	36	9	AZ796083
92	11	4.4	36	9	CG723596
93	11	4.4	37	1	AI574257
94	11	4.4	37	1	AI636412
95	11	4.4	37	7	AA238798
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AI431129	sa22601.Y
AI580030	lq45f02.x
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AI558328	fb78908.x
AI803362	lc3812.x
BZ595573	SALK_0891
CG730671	1119129A0
CL528564	ASV20E06.
AI462129	ub70d04.x
AI918475	lc31e03.x
CB275442	WLR151-15
CF301504	7LEAF--06
BH855386	SALK_0858
AI359255	qy27a11.x
AI471547	cl96f04.x
AI627640	ly81a12.x
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AV851415	AV851415
AI367375	qv95f07.x
AZ400633	IM0167F06
AI490332	T. brucei
AU103657	AU103657
AU105195	AU105195
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AU105435	AU105435
AU105888	AU105888
AZ637037	IM0496C19
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AJ685570	AJ685570
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AZ785173	2M0028G19
TA178F08P	T. brucei
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BM393952	50072-2-1
AZ408503	IM0179P12
AZ514561	IM0361N07
AZ588957	IM0397B08
AA968474	OP49f06..8
AI032807	ox19609..8
AI460125	ar79b03.x
AI475457	l18h01.x
AI917527	co27b02.x
AZ490711	IM0323B24
AZ936441	2M0193E07
BG970134	602839265
AZ492861	1M0327D24
AZ783039	2M0024H20
AI679919	cn65f04.x
AI679919	tu67d10..x
AZ628045	IM0476C24
AZ628045	2M0102P11
AZ628045	2M0204G02
AZ936441	SAIX_0628
BH792156	AV832693
BM400381	5009-0-72
AZ469734	1M0283J19
AZ796083	2M0051G03
CG723596	1119077B0
AI574257	u119d11.x
AI636412	cz79609.x
AA238798	mx93c01..r
H23949	yn75f10..s1
AZ615410	IM0444C13

98 11 4.4 38 8 BH792213
99 11 4.4 38 9 AJ595806
c 100 11 4.4 39 8 AZ833920
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ALIGNMENTS

RESULT 1
LOCUS BU052484 45 bp mRNA linear EST 29-SEP-2003
DEFINITION BU052484 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL041k15 3', mRNA sequence.
ACCESSION BU052484
VERSION BU052484.1 GI:17498532
KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 45)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.

FEATURES
source Location/Qualifiers
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/organism="Xenopus laevis"
/mol_type="mRNA"
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/clone="XL041k15"
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/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 GGGGGGGCTTTCTG 36
DB 14 GGGGGGGCTTTCTG 28

RESULT 2
LOCUS AU105461 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU105461 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC02754, mRNA sequence.
ACCESSION AU105461
VERSION AU105461.1 GI:13554982
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 GACGAGACGAGGC 161
DB 8 GACGAGACGAGGC 21

RESULT 3
LOCUS AU105462 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU105462 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC05718, mRNA sequence.
ACCESSION AU105462
VERSION AU105462.1 GI:13554983
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 5.6%; Score 14; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 263.946 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-8

Perfect score: 251
Sequence: 1 59CG9GCGCGGCGCGCGG.....CGTCCCGCCGCGTGTGT 251

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

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7: geneseqn2002bs:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	15	6.0	34	4	AA501435 Hepatitis
4	15	6.0	40	2	AAT97484 Productio
5	15	6.0	40	3	AAZ95304 Polynucle
6	15	5.6	20	12	ADM15539 Human m1g
7	15	5.6	20	12	ADM15583 Human m1g
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12	15	5.6	20	12	ADM15587 Human m1g
13	15	5.6	30	2	AAT45866 Primer to
14	15	5.6	32	3	AAZ46076 PCR prime
15	15	5.6	34	6	AA14532 Azole com
16	15	5.6	34	9	ADA37010 Human c1u
17	15	5.6	34	12	ADQ26017 C-Jun-N-t
18	15	5.6	41	6	ABL54610 Human syn
19	15	5.6	50	2	AAQ69634 Human alp
20	15	5.6	50	2	AAT64096 Human alp

21	14	5.6	50	2	AAK17384	AAK17384 Test sequ
22	14	5.6	50	6	ABK82875	ABK82875 DNA bindi
23	14	5.6	50	12	AD880414	AD880414 Duplex ol
24	13	5.2	14	12	AD078064	AD078064 Human MxA
25	13	5.2	15	10	ABX08694	ABX08694 Patchogeni
26	13	5.2	15	12	ADL72195	ADL72195 Human nuc
27	13	5.2	15	12	ADM30871	ADM30871 Escherich
28	13	5.2	15	12	ADM30869	ADM30869 Escherich
29	13	5.2	15	12	ADM79790	ADM79790 Human DNA
30	13	5.2	15	12	AD078065	AD078065 Human MxA
31	13	5.2	17	2	AAK73045	AAK73045 Mouse. f1k
32	13	5.2	17	8	ABT36128	ABT36128 Tumour su
33	13	5.2	18	2	AAK73494	AAK73494 Mouse f1k
34	13	5.2	18	10	ADG98222	ADG98222 Cancer de
35	13	5.2	19	10	ABX08689	ABX08689 Pathogeni
36	13	5.2	19	11	AD015168	AD015168 Human PDG
37	13	5.2	19	11	AD014857	AD014857 Human PDG
38	13	5.2	20	2	AAQ73341	AAQ73341 Anti-HSV-
39	13	5.2	20	2	AAQ61978	AAQ61978 HSV detec
40	13	5.2	20	2	AAQ55818	AAQ55818 HCV detec
41	13	5.2	20	4	AAQ82158	AAQ82158 Chromosom
42	13	5.2	20	4	AAQ19517	AAQ19517 PBADGFP4
43	13	5.2	20	10	ADH94413	ADH94413 Human gen
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50	13	5.2	20	12	ADM15197	ADM15197 Human m1g
51	13	5.2	20	12	ADO45747	ADO45747 Human o1i
52	13	5.2	21	6	ABK29183	ABK29183 Penicill1i
53	13	5.2	21	6	ABN9586	ABN9586 Fungi PCR
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65	13	5.2	26	5	AA822046	AA822046 Human COL
66	13	5.2	28	2	AAQ87359	AAQ87359 Human IGM
67	13	5.2	28	2	AAQ82511	AAQ82511 Human IGM
68	13	5.2	28	2	AAV66888	AAV66888 Human imm
69	13	5.2	28	2	AAV37305	AAV37305 PCR prime
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72	13	5.2	32	2	AAV33798	AAV33798 RT-PCR pr
73	13	5.2	33	6	ABK47960	ABK47960 Human lar
74	13	5.2	36	12	ADL70692	ADL70692 Helicobac
75	13	5.2	39	12	ADM13507	ADM13507 GFP ciru
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77	13	5.2	40	4	AAV10787	AAV10787 S. clauv1
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79	13	5.2	40	4	AAV10787	AAV10787 S. clauv1
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81	13	5.2	41	6	ABK47962	ABK47962 Human lar
82	13	5.2	41	6	ABZ50624	ABZ50624 Human lar
83	13	5.2	42	12	ADP48416	ADP48416 Human car
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86	13	5.2	45	2	AAV02625	AAV02625 Primer 26
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88	13	5.2	47	10	ADP32426	ADP32426 Oligonuc1
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92	13	5.2	50	2	AAQ69580	AAQ69580 Human h1s
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ALIGNMENTS

RESULT 1

ACI84515/c

ID ACI84515 standard; DNA; 25 BP.

AC ACI84515;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 84506.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;

KW genetic variation; biallelic marker; polymorphism; human;

KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PR 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in

PT Southern, Northern or dot-blot hybridization to identify or detect the

PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 84506; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' terminus of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 6 A; 4 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 6.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 AGTCATGACCCANA 215
DB 17 AGTCATGACCCANA 3

RESULT 2

ADN95072

ID ADN95072 standard; DNA; 28 BP.

AC ADN95072;

DT 29-JUL-2004 (first entry)

DE Human CYP2W1 PCR primer SEQ ID NO:7.

KW cytotoxic; anti-cancer; cytochrome P450 enzyme; CYP2W1; enzyme;

KW cancer therapy; drug target; lung tumour; colon tumour; ovarian tumour;

KW cancer; human; PCR; primer; ss.

OS Homo sapiens.

PN WO2004037282-A1.

PD 06-MAY-2004.

PR 24-OCT-2003; 2003WO-SE001652.

PR 24-OCT-2002; 2002SE-00003137.

PR 24-OCT-2002; 2002US-0420787P.

PA (KARO-) KAROLINSKA INNOVATIONS AB.

PI Ingelman-Sundberg M, Karlgren M, Gomez A;

DR WPI; 2004-389744/36.

PT New compound comprising a part conferring cytotoxic and/or anti-cancer

PT effects, and one part conferring binding affinity towards cytochrome P450

PT enzyme CYP2W1 to the compound, useful in screening agents for treating

PT cancer.

PS Disclosure; SEQ ID NO 7; 46pp; English.

The present invention describes a compound (I) comprising one part conferring cytotoxic and/or anti-cancer effects to the compound and one part conferring binding affinity towards cytochrome P450 enzyme CYP2W1 to the compound. Also described: (1) a pharmaceutical composition comprising (I), and pharmaceutical excipients and/or carrier; (2) an antibody, (3) a preferably a monoclonal antibody, binding specifically to CYP2W1; (4) a DNA molecule having a 137 bp nucleotide sequence of SEQ ID NO:10 (ADN95075); and (4) a method of providing therapeutic agents for cancer therapy, comprising screening for such agents by using CYP2W1 as a drug target, or screening for such agents modulating expression of genes regulated by the CYP2W1 promoter comprising SEQ ID NO:10. The cytochrome P450 enzyme CYP2W1 and its genetic variants are useful as a drug target in cancer therapy, preferably in the treatment of lung tumours, colon tumour and/or ovarian tumours. The substance activated by the enzyme, CYP2W1 and/or inducing the enzyme CYP2W1, and/or the compound above, is useful for treating cancer. The DNA is useful in the manufacture of a medicament. The cytochrome P450 form, CYP2W1, has recently been found to be mainly expressed in tumour cells and is so can be a new potential agent for effective cancer therapy by acting as a drug target. By targeting cancer products to CYP2W1, they can be metabolically activated by the enzyme into the cytotoxic form and reduce unwanted systemic effects of toxic drugs. The present sequence represents a PCR primer for human CYP2W1, which is used in the exemplification of the present invention.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1540.09 Seconds
(without alignments)
7897.122 Million cell updates/sec

Title: US-09-887-941B-8

Perfect score: 251

Sequence: 1 ggcggcgctggcgacgcgcg.....cgttccccaccgtgtgtc 251

Scoring table: ORIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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3: gb_in:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	15	6.0	40	6	172157 Sequence 14
C 3	14	5.6	30	6	126210 Sequence 7
C 4	14	5.6	30	7	162910 Sequence 14
C 5	14	5.6	34	6	BD173847 JNK Inhib
C 6	14	5.6	50	6	AR032772 Sequence 38
C 7	14	5.6	50	6	129512 Sequence 38
C 8	14	5.6	50	6	AR209436 Sequence 38
C 9	14	5.6	50	6	AR209436 Sequence 38
C 10	13	5.2	15	6	BD178522 Method of
C 11	13	5.2	15	6	BD182915 Detection
C 12	13	5.2	17	6	AR190307 Sequence
C 13	13	5.2	17	6	AR325259 Sequence
C 14	13	5.2	17	6	AX730131 Sequence
C 15	13	5.2	18	6	AR190756 Sequence
C 16	13	5.2	18	6	AR325602 Sequence
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99 12 4.8 21 6 AR411352 AR411352 Sequence
100 12 4.8 21 6 AX394247 AX394247 Sequence

ALIGNMENTS

RESULT 1
LOCUS I70176/c 170176 40 bp DNA linear PAT 02-APR-1998
DEFINITION Sequence 14 from patent US 5679512.
ACCESSION I70176
VERSION I70176.1 GI:3006311
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Loney,M., Chen,Y., Ullman,E.F. and Hahnenberger,K.M.
TITLE Method for introducing defined sequences at the 3' end of
JOURNAL polynucleotides
FEATURES
PATENT: US 5679512-A 14 21-OCT-1997;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GGGGGGGCTTTCTG 36
DB 28 GGGGGGGCTTTCTG 14

RESULT 2
LOCUS I72157/c 172157 40 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 14 from patent US 5683879.
ACCESSION I72157
VERSION I72157.1 GI:3008296
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Loney,M., Chen,Y., Ullman,E.F. and Hahnenberger,K.M.
TITLE Method for producing a single stranded polynucleotide having
JOURNAL two different defined sequences and kits
FEATURES
PATENT: US 5683879-A 14 04-NOV-1997;
Location/Qualifiers
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ORIGIN
Query Match 6.0%; Score 15; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GGGGGGGCTTTCTG 36
DB 28 GGGGGGGCTTTCTG 14

RESULT 3
LOCUS I26210/c 126210 30 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 7 from patent US 5556953.
ACCESSION I26210
VERSION I26210.1 GI:1606080
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Zhang,L., Vijay,H.M. and Rode,H.
TITLE Allergen of despositum herbarum
JOURNAL Patent: US 5556953-A 7 17-SEP-1996;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 5.6%; Score 14; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 GACGGTGTGCTTTCG 11

RESULT 4
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DEFINITION Bacteriophage fd (clone RDEC29) DNA fragment.
ACCESSION L07985
VERSION L07985.1 GI:1246245
KEYWORDS
SOURCE Enterobacteria phage fd
ORGANISM Enterobacteria phage fd
REFERENCE 1 (bases 1 to 30)
AUTHORS Degraef,M.E., Miceli,R.M., Mott,J.E. and Fischer,H.D.
TITLE Biochemical diversity in a phage display library of random
JOURNAL decapeptides
MEDLINE Gene 128 (1), 13-17 (1993)
PUBMED 93285461
COMMENT Original source text: Coliphage fd (clone: RDEC29) DNA.
FEATURES
Location/Qualifiers
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/db_xref="taxon:10864"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ACAGGGCATGGCAC 168
DB 29 ACAGGGCATGGCAC 16

RESULT 5
LOCUS BD173847/c BD173847 34 bp DNA linear PAT 18-FEB-2003
DEFINITION JNK inhibitor.
ACCESSION BD173847
VERSION BD173847.1 GI:28415180
KEYWORDS WO 02062792-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct

QY 22 GGGGGGGCTTTCTG 36
DB 28 GGGGGGGCTTTCTG 14

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Title: US-09-887-941B-7

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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8	14	3.9	25	4	US-09-396-196G-5567
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13	14	3.9	25	4	US-09-396-196G-104809
14	14	3.9	25	4	US-09-396-196G-104810
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c 29	13	3.6	21	4	US-09-492-361-25	Sequence 25, Appl
c 30	13	3.6	24	3	US-09-079-984A-4	Sequence 4, Appl
c 31	13	3.6	24	4	US-09-390-729-4	Sequence 4, Appl
c 32	13	3.6	25	1	US-07-924-063A-8	Sequence 8, Appl
c 33	13	3.6	25	4	US-09-396-196G-985	Sequence 985, App
c 34	13	3.6	25	4	US-09-396-196G-986	Sequence 986, App
c 35	13	3.6	25	4	US-09-396-196G-987	Sequence 987, App
c 36	13	3.6	25	4	US-09-396-196G-5003	Sequence 5003, Ap
c 37	13	3.6	25	4	US-09-396-196G-5568	Sequence 5568, Ap
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c 61	13	3.6	30	4	US-08-442-423-48	Sequence 42, Appl
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c 63	13	3.6	33	4	US-09-339-922A-43	Sequence 43, Appl
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c 65	13	3.6	33	4	US-09-016-061-43	Sequence 43, Appl
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c 84	13	3.6	42	3	US-09-306-405-72	Sequence 72, Appl
c 85	13	3.6	42	3	US-09-455-061-40	Sequence 40, Appl
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c 89	13	3.6	44	1	US-08-122-433-10	Sequence 10, Appl
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c 91	13	3.6	44	4	US-08-339-159B-53	Sequence 53, Appl
c 92	13	3.6	46	4	US-09-422-978-913	Sequence 913, App
c 93	13	3.6	47	4	US-08-701-124-38	Sequence 38, Appl
c 94	13	3.6	48	2	US-09-130-225-38	Sequence 38, Appl
c 95	13	3.6	48	3	US-09-455-061-38	Sequence 38, Appl
c 96	13	3.6	48	3	US-09-969-192-38	Sequence 38, Appl
c 97	13	3.6	50	1	US-08-171-189-407	Sequence 407, App
c 98	13	3.6	50	1	US-08-123-926-407	Sequence 407, App
c 99	13	3.6	50	2	US-08-475-228A-407	Sequence 407, App
c 100	13	3.6	50	2	US-08-475-228A-407	Sequence 407, App

ALIGNMENTS

RESULT 1
US-08-584-040-5702
; Sequence 5702, Application US/08584040
; Patent No. 6346359
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 216/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-5702

Query Match 3.9%; Score 14; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 248 TGAACCTAGAGAAA 261
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Db 2 UGAAACUAGAGAAA 15

RESULT 2
US-09-371-772B-2586
; Sequence 2586, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2586
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2586

Query Match 3.9%; Score 14; DB 4; Length 17;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 248 TGAACCTAGAGAAA 261
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Db 2 UGAAACUAGAGAAA 15

RESULT 3
US-09-685-664B-2586
; Sequence 2586, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2586
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2586

Query Match 3.9%; Score 14; DB 4; Length 17;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 248 TGAACCTAGAGAAA 261
:||||:|||||
Db 2 UGAAACUAGAGAAA 15

RESULT 4
US-09-269-446D-127
; Sequence 127, Application US/09269446D
; Patent No. 6825332
; GENERAL INFORMATION:
; APPLICANT: Frants, Rune Robert Isak Erik

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 2497.01 Seconds
(without alignments)
5472.564 Million cell updates/sec

Title: US-09-887-941B-7

Perfect score: 359
Sequence: 1 ccccgcgggcgagaccacaa.....tcacctgcctcgcgcgcgcg

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database:

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4.2	43	8	AZ647300	IM0513B15
2	3.9	31	1	AA909441	AA909441
3	3.9	35	8	AZ630264	IM0483F14
4	3.9	49	8	AZ788244	2M0035O10
5	3.6	27	8	BZ354127	SAUK_1232
6	3.6	30	9	AG199320	Pan trogl
7	3.6	30	9	AL946879	Arabidops
8	3.6	31	9	TA9D04P	AL946879
9	3.6	32	8	BH908757	AL946879
10	3.6	34	4	AA277392	T. brucei
11	3.6	37	8	AJ590063	Arabidops
12	3.6	37	8	AZ666463	IM0548D08
13	3.6	41	8	AL978148	AL978148
14	3.6	46	1	AL978148	AL978148
15	3.6	19	8	AZ995149	AL978148
16	3.3	20	8	AZ434383	2M0280D22
17	3.3	22	7	CP300339	2M0280D22
18	3.3	22	7	CP300339	2M0280D22
19	3.3	25	1	AU257461	2M0280D22
20	3.3	25	1	AU257461	2M0280D22
21	3.3	27	7	CG708283	2M0280D22
22	3.3	27	7	CG708283	2M0280D22
23	3.3	29	6	CA851403	2M0280D22
24	3.3	29	6	AZ387151	2M0280D22

25	12	3.3	29	9	CL439335	PST9058-N
26	12	3.3	31	1	AI032592	OW73G08.B
27	12	3.3	31	1	CG719539	1119058A1
28	12	3.3	31	9	CL435872	PST1677-2
29	12	3.3	34	1	AA885809	OJ35C10.S
30	12	3.3	34	8	AZ592538	IM0403H02
31	12	3.3	35	7	CF298614	7LEAF--02
32	12	3.3	37	7	AA877091	OB09C09.S
33	12	3.3	37	7	H28311	Y160D11.S1
34	12	3.3	37	8	AZ366273	IM0151L16
35	12	3.3	37	8	AZ663202	IM0542P08
36	12	3.3	38	8	AZ775203	2M0007C24
37	12	3.3	39	8	AZ450000	IM0246H06
38	12	3.3	40	1	AA848120	OE05A03.S
39	12	3.3	40	1	AA887375	OJ35G08.S
40	12	3.3	40	9	AG203784	Pan trogl
41	12	3.3	40	9	AG203784	Pan trogl
42	12	3.3	41	8	AZ662472	IM0541A09
43	12	3.3	41	8	AZ662472	IM0541A09
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45	12	3.3	41	8	AZ662472	IM0541A09
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57	12	3.3	41	8	AZ662472	IM0541A09
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59	12	3.3	41	8	AZ662472	IM0541A09
60	12	3.3	41	8	AZ662472	IM0541A09
61	12	3.3	41	8	AZ662472	IM0541A09
62	12	3.3	41	8	AZ662472	IM0541A09
63	12	3.3	41	8	AZ662472	IM0541A09
64	12	3.3	41	8	AZ662472	IM0541A09
65	12	3.3	41	8	AZ662472	IM0541A09
66	12	3.3	41	8	AZ662472	IM0541A09
67	12	3.3	41	8	AZ662472	IM0541A09
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69	12	3.3	41	8	AZ662472	IM0541A09
70	12	3.3	41	8	AZ662472	IM0541A09
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76	12	3.3	41	8	AZ662472	IM0541A09
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78	12	3.3	41	8	AZ662472	IM0541A09
79	12	3.3	41	8	AZ662472	IM0541A09
80	12	3.3	41	8	AZ662472	IM0541A09
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82	12	3.3	41	8	AZ662472	IM0541A09
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84	12	3.3	41	8	AZ662472	IM0541A09
85	12	3.3	41	8	AZ662472	IM0541A09
86	12	3.3	41	8	AZ662472	IM0541A09
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89	12	3.3	41	8	AZ662472	IM0541A09
90	12	3.3	41	8	AZ662472	IM0541A09
91	12	3.3	41	8	AZ662472	IM0541A09
92	12	3.3	41	8	AZ662472	IM0541A09
93	12	3.3	41	8	AZ662472	IM0541A09
94	12	3.3	41	8	AZ662472	IM0541A09
95	12	3.3	41	8	AZ662472	IM0541A09
96	12	3.3	41	8	AZ662472	IM0541A09
97	12	3.3	41	8	AZ662472	IM0541A09

98 11 3.1 27 9 AG195526 AG195526 Pan tlog1
 c 99 11 3.1 27 9 TA128C06P AL64342 T. brucei
 100 11 3.1 27 9 CC887313 CC887313 SALK_1499

ALIGNMENTS

RESULT 1
 LOCUS AZ647300/c 43 bp DNA linear GSS 14-DEC-2000
 DEFINITION 1M051B15R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0513B15 R, genomic survey sequence.

ACCESSION AZ647300
 VERSION AZ647300.1 GI:11778628
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 43)
 Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunham@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0513 row: B column: 15
 Seq primer: CACACAGCAACACGTATGACC
 Class: plasmid ends
 High quality sequence stop: 43.

FEATURES
 source
 1. 43
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0513B15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g114732114[gD]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 4.2%; Score 15; DB 8; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 333 GTTCTCATCACCCTGC 347
 Db 36 GTTCTCATCACCCTGC 22

RESULT 2
 LOCUS AA909441 31 bp mRNA linear EST 10-JUN-1998
 DEFINITION 0114C09.01 Soares NFL T GBC S1 Homo sapiens cDNA clone
 IMAGE:1523440 3' similar to TR:035606 035606 HYPOTHETICAL 35.7 KD
 PROTEIN ; mRNA sequence.

ACCESSION AA909441
 VERSION AA909441.1 GI:3048846
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 31)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Straubeberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 645 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 31
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1523440"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBH19w, testis NHT, and B-cell
 NCI-CCAP GC81) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.9%; Score 14; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.4e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AAGTGAGTCAGACA 32
 Db 4 AAGTGAGTCAGACA 17

RESULT 3
 LOCUS AZ630264 35 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0483P14R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0483P14 R, genomic survey sequence.

ACCESSION AZ630264
 VERSION AZ630264.1 GI:11752454
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

PR 08-JAN-2001; 2001US-0260326P.
 PR 24-JAN-2001; 2001US-0263800P.
 PR 20-FEB-2001; 2001US-0269942P.
 PR 24-APR-2001; 2001US-0286183P.
 PR 20-AUG-2001; 2001US-0313627P.
 PR 12-SEP-2001; 2001US-0318712P.

XX (CURA-) CURAGEN CORP.

PI Guo X, Li L, Patturajan M, Shinkets RA, Casman SJ, Malayankar UM;
 PI Tcherev VT, Vernet CM, Spytek KA, Shenoy SG, Alsobrook JP;
 PI Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FL;
 PI Colman SD, Eissen AJ, Liu X, Padigaru M, Spaderna SK, Zehusen BD;
 XX WPI; 2002-547774/58.

XX Novel isolated polypeptide, designated NOVX, useful for treating or
 PT preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and
 PT metabolic, neurodegenerative, immune and hematopoietic disorders.

XX Example 2; Page 331; 421pp; English.

XX The invention relates to an isolated polypeptide, designated NOVX,
 CC comprising a sequence fully defined in the specification. The isolated
 CC protein, its encoding polynucleotide or an antibody created from the
 CC protein is useful in the manufacture of a medicament for treating a
 CC syndrome associated with a human disease, preferably a NOVX-associated
 CC disorder, or for treating or preventing a NOVX-associated disorder in a
 CC subject, preferably human. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are also useful
 CC for treating or preventing metabolic disorders, diabetes, obesity,
 CC infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
 CC disease, Parkinson's disorder, immune disorders, haematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, the metabolic syndrome X, wasting disorders associated with
 CC chronic diseases, and cancer. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are useful for
 CC treating or preventing neurological disorders such as epilepsy, stroke,
 CC mental disorders including mood, anxiety, schizophrenic disorders,
 CC disorders of vesicular transport such as cystic fibrosis, diabetes
 CC mellitus, golfer, gastrointestinal disorders including ulcerative
 CC colitis, other conditions associated with abnormal vesicle trafficking
 CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid
 CC arthritis. A cell comprising the vector of the invention is useful for
 CC producing non-human transgenic animals. The polynucleotide of the
 CC invention can be used to treat disorders by gene therapy. This
 CC polynucleotide sequence represents a probe of a sequence relating to the
 CC NOVX proteins of the invention

XX Sequence 23 BP; 2 A; 10 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 4.5%; Score 16; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TCCCTCCCTGCTGCTG 54
 |||||
 DB 8 TCCCTCCCTGCTGCTG 23

RESULT 4

ID ACI09033/c
 ACI09033 standard; DNA; 25 BP.

XX ACI09033;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 9024.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; diallelic marker; polymorphism; human;
 KW cross-species comparison.

XX Homo sapiens.

XX US200104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFY-) AFFYMETRIX INC.

XX Miltmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 9024; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 4 A; 10 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 4.5%; Score 16; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 TCAGAAAGGCTGAGAG 231
 |||||
 DB 16 TCAGAAAGGCTGAGAG 1

RESULT 5

ID ACH56901/c
 ACH56901 standard; DNA; 25 BP.

XX ACH56901;

XX 16-OCT-2003 (first entry)

XX DNA target sequence #6037 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;
 KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.

XX OS Unidentified.
XX PN US2003082596-A1.
XX XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mitmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
PS
PS Claim 1; SEQ ID NO 6037; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/patidbIDEntry.html
XX
XX Sequence 25 BP; 8 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 4.5%; Score 16; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 295 ACACACTGCTTCTGCT 310
Db 23 ACACACTGCTTCTGCT 8
RESULT 6
ACH56902/C
ID ACH56902 standard; DNA; 25 BP.
XX
XX ACH56902;
AC
DT 16-OCT-2003 (first entry)
XX
XX DNA target sequence #6038 useful in array for genetic analyses.
XX
XX Gene expression analysis: array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.

XX OS Unidentified.
XX PN US2003082596-A1.
XX XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mitmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
PS
PS Claim 1; SEQ ID NO 6038; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/patidbIDEntry.html
XX
XX Sequence 25 BP; 8 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 4.5%; Score 16; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 295 ACACACTGCTTCTGCT 310
Db 23 ACACACTGCTTCTGCT 8
RESULT 7
AD150603
ID AD150603 standard; DNA; 17 BP.
XX
XX AD150603;
AC
DT 15-APR-2004 (first entry)
XX
XX Human tumour suppression/reversion-related DNA sequence SeqID1106.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytoskeletal; virucide; neuroprotective; neurotropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 377.516 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-7

Perfect score: 359
Sequence: 1 cccgcggggcagcgaatccaa.....tcacctgcctcgcgcgccgc 359

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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10: geneseqn2003cs:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	4.7	30	2	AAQ10507
2	16	4.5	20	12	ADK96823
3	16	4.5	23	6	ABT05541
4	16	4.5	23	6	ACT09033
5	16	4.5	25	9	ACH56901
6	16	4.5	25	9	ACH56902
7	15	4.2	17	10	AD150603
8	15	4.2	19	12	AD016727
9	15	4.2	20	6	AA147253
10	15	4.2	48	10	ACH01195
11	15	4.2	48	10	ACH01186
12	15	4.2	50	6	AB202647
13	14	3.9	15	2	AA776266
14	14	3.9	15	2	AA554056
15	14	3.9	15	3	AAA33500
16	14	3.9	15	3	AA19622
17	14	3.9	15	3	ABZ95316
18	14	3.9	15	11	ABD19300
19	14	3.9	17	2	AA72952
20	14	3.9	18	4	AA08679

C	21	14	3.9	19	10	ADP37166	Adf37186 Human VEG
C	22	14	3.9	19	10	ADP36862	Adf36862 Human VEG
C	23	14	3.9	20	2	AAV29457	Aav29457 Calcium i
C	24	14	3.9	21	2	AA740022	Aat40022 Primer fo
C	25	14	3.9	21	6	AA518347	Aa518347 5'-RACE h
C	26	14	3.9	22	3	AAA66353	Aaa66353 Dog genom
C	27	14	3.9	22	3	AB279337	Ab279337 Acetyl-Co
C	28	14	3.9	25	9	ACT18925	Act18925 Human mtc
C	29	14	3.9	25	9	ACK09568	Ack09568 Human mtc
C	30	14	3.9	25	9	ACK18741	Ack18741 Human mtc
C	31	14	3.9	25	9	ACK18734	Act18734 Human mtc
C	32	14	3.9	25	9	ACT176389	Act176389 Human mtc
C	33	14	3.9	28	12	ADN43292	Adn43292 Nucleotici
C	34	14	3.9	28	12	ADN43291	Adn43291 Nucleotici
C	35	14	3.9	30	2	AA710251	Aat10251 Human Fas
C	36	14	3.9	30	12	AA156358	Aa156358 Human pro
C	37	14	3.9	33	9	ACC49573	Acc49573 Beta-cong
C	38	14	3.9	33	9	AA156359	Aa156359 Human pro
C	39	14	3.9	40	12	AA156359	Abx15068 Homeotic
C	40	14	3.9	41	6	AA15068	Abx15068 Homeotic
C	41	14	3.9	44	4	AA15068	Abx15068 Homeotic
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C 94 13 3 6 21 9 ACD26205
95 13 3 6 21 10 AD42650
96 13 3 6 21 12 AD85723
97 13 3 6 22 2 ADG77609
98 13 3 6 22 12 AD018066
99 13 3 6 22 13 AD017994
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ALIGNMENTS

RESULT 1

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AAQ10507
ID AAQ10507 standard; DNA; 30 BP.

```

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AC AAQ10507;
DT 09-APR-1991 (first entry)

```

```

XX 5' primer (87-311) for amplification of male-specific bovine DNA.

```

```

XX bovine; sex determination; male-specific probe; PCR; ss.

```

```

XX Synthetic.

```

```

XX MO9100365-A.

```

```

XX 10-JAN-1991.

```

```

XX 13-JUN-1989; 89US-00366153.

```

```

XX 13-JUN-1989; 89US-00366153.

```

```

XX (SALK ) SALK INST BIOTECHN.

```

```

XX Kwok DY, Gingeras T;

```

```

XX WPI; 1991-036756/05.

```

```

XX Prenatal bovine sex determ. - using male-specific oligo-nucleotide
XX probes, with increased sensitivity.

```

```

XX Claim 8; Page 31; 40pp; English.

```

```

CC This 5' primer is used in association with a 3' primer (AAQ10508) and a
CC detection oligonucleotide (AAQ10509) in a sex-determination assay. A male
CC -specific segment of bovine DNA is amplified by using the primers in a
CC Polymerase Chain Reaction. The amplified, double-stranded male-specific
CC segment is then detected by hybridisation between the DNA and the
CC specified probe. See also AAQ10504-6 and AAQ10510-18

```

```

XX Sequence 30 BP; 10 A; 13 C; 4 G; 3 T; 0 U; 0 Other;

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XX Query Match 4.7%; Score 17; DB 2; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 3e+02;

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XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 170 CTGACAAACACTCTCTGA 186
Db 7 CTGACAAACACTCTCTGA 23

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RESULT 2
ADK96823/c
ID ADK96823 standard; DNA; 20 BP.

```

```

XX ADK96823;

```

```

XX 06-MAY-2004 (first entry)

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XX Primer of the invention #2543.

```

```

KW human; single nucleotide polymorphism; SNP; ss; primer.

```

```

XX Synthetic.

```

```

XX JP2003259875-A.

```

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XX 16-SEP-2003.

```

```

XX 08-MAR-2002; 2002JP-00064373.

```

```

XX 08-MAR-2002; 2002JP-00064373.

```

```

XX (KAGA-) KAGAKU GIYUSU SHINKO JIGYODAN.

```

```

XX WPI; 2004-093977/10.

```

```

XX Novel polynucleotide useful for PCR amplification along with two DNA
XX fragment from another set of sequences, or for detecting single
XX nucleotide polymorphism in human gene.

```

```

XX Claim 2; SEQ ID NO 5852; 2627bp; Japanese.

```

```

CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.

```

```

XX Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

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XX Query Match 4.5%; Score 16; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;

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XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 142 AGAGGGCACAGATGCT 157
Db 17 AGAGGGCACAGATGCT 2

```

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RESULT 3
ABT05541
ID ABT05541 standard; DNA; 23 BP.

```

```

XX ABT05541;

```

```

XX 11-OCT-2002 (first entry)

```

```

XX NOVA related probe SEQ ID No 215.

```

```

KW Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antihypertic;
KW neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
KW tranquiliser; neuroleptic; antidiabetic; antitumor; antiinflammatory;
KW anti-HIV; antiallergic; antirheumatic; antirheumatic; NOVA; diabetes;
KW metabolic disorder; obesity; infectious disease; Alzheimer's disease;
KW anorexia; neurodegenerative disorder; Parkinson's disease; obesity;
KW immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
KW metabolic syndrome X; wasting disorder; cancer; neurological disorder;
KW epilepsy; stroke; mental disorder; schizophrenic disorders; golfer;
KW vesicular transport; cystic fibrosis; gastrointestinal disorder;
KW diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
KW multiple sclerosis; rheumatoid arthritis; transgenic animal;
KW gene therapy; probe; ss.

```

```

XX Unidentified.

```

```

XX WO200246409-A2.

```

```

XX 13-JUN-2002.

```

```

XX 06-DEC-2001; 2001WO-US046586.

```

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XX 06-DEC-2000; 2000US-0251660P.
XX 12-DEC-2000; 2000US-0255029P.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
7897.122 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

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Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	14	3.9	17	6	AR190214 Sequence
4	14	3.9	17	6	AR325184 Sequence
5	14	3.9	18	6	AX189329 Sequence
6	14	3.9	20	6	A70806 Sequence 12
7	14	3.9	20	6	A79290 Sequence 12
8	14	3.9	20	6	BD003520 A gene re
9	14	3.9	21	6	AR142730 Sequence
10	14	3.9	21	6	AR560775 Sequence
11	14	3.9	21	6	AX299993 Sequence
12	14	3.9	22	6	BD230346 Total gen
13	14	3.9	22	6	AX657311 Sequence
14	14	3.9	30	6	AX959246 Sequence
15	14	3.9	33	11	AL824241 Arabidops
16	14	3.9	40	6	AX959247 Sequence
17	14	3.9	50	5	XLRGRT2A
18	13	3.6	17	6	BD197447 Method an
19	13	3.6	17	6	AX725139 Sequence
20	13	3.6	18	6	BD103977 Kit and m
21	13	3.6	18	6	BD104423 Kit and m
22	13	3.6	19	6	AX645147 Sequence
23	13	3.6	19	6	AX645150 Sequence
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25	13	3.6	20	6	126471 Sequence 16
26	13	3.6	20	6	AR229043 Sequence
27	13	3.6	20	6	AR243614 Sequence
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29	13	3.6	20	6	AR315961 Sequence
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32	13	3.6	20	6	AX613685 Sequence
33	13	3.6	20	6	AX696254 Sequence
34	13	3.6	21	6	AR123316 Sequence
35	13	3.6	21	6	105464 Sequence 1
36	13	3.6	21	6	AR487412 Sequence
37	13	3.6	21	6	AX033018 Sequence
38	13	3.6	21	6	AX060890 Sequence
39	13	3.6	23	6	AX181761 Sequence
40	13	3.6	23	6	AX921463 Sequence
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45	13	3.6	24	6	BD014656 Process f
46	13	3.6	25	6	C0864984 Sequence
47	13	3.6	25	6	E55245 Thermophil
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50	13	3.6	28	6	AR533403 Sequence
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54	13	3.6	30	6	AR125706 Sequence
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56	13	3.6	30	6	147118 Sequence 48
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62	13	3.6	33	6	AR360821 Sequence
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73	13	3.6	34	6	AX002913 Sequence
74	13	3.6	34	6	AX018239 Sequence
75	13	3.6	36	6	AR160940 Sequence
76	13	3.6	36	6	116111 Sequence 18
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ALIGNMENTS

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 VERSION AX591854.1 GI:27950124
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS

synthetic construct
 synthetic construct
 other sequences; artificial sequences.

1
 Guo,X., Li,L., Patturajan,M., Shinkens,R.A., Casman,S.J.,
 Malyanar,U.M., Tchernev,V.T., Vernet,C.A., Spytek,K.A.,
 Shenoy,S.G., Alsbrook,J.P., Edinger,S., Peyman,J.A., Stone,D.J.,
 Ellerman,K., Gangoli,E.A., Boldog,F.L., Colman,S.D., Eisen,A.D.,
 Liu,X., Padigaru,M., Spaderna,S.K. and Zerhusen,B.D.
 Proteins and nucleic acids encoding same
 Patent: WO 0246409-A 215 13-JUN-2002;
 Curegen Corporation (US)
 Location/Qualifiers

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 DEFINITION Sequence 3106 from Patent WO03025177.
 ACCESSION AX737516
 VERSION AX737516.1 GI:30516804
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
 Telemann,A., Amsen,R. and Tuijinder,M.
 Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or resistance to viruses and the use
 thereof as medicaments
 Patent: WO 03025177-A 3106 27-MAR-2003;

JOURNAL Molecular Engines Laboratories (FR)
 Location/Qualifiers

FEATURES
 source

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 DB 3 TCAGACACATTGCTC 17

RESULT 3
 AR190214 17 bp DNA linear PAT 20-APR-2002
 LOCUS AR190214
 DEFINITION Sequence 5702 from patent US 6346398.
 ACCESSION AR190214
 VERSION AR190214.1 GI:20236179
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 ORGANISM

Unknown.
 Unknown.
 Unclassified.

REFERENCE
 Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
 Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 Patent: US 6346398-A 5702 12-FEB-2002;
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RESULT 4
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 LOCUS AR325184
 DEFINITION Sequence 2586 from patent US 6566127.
 ACCESSION AR325184
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 KEYWORDS
 SOURCE
 ORGANISM

Unknown.
 Unknown.
 Unclassified.

REFERENCE
 1 (bases 1 to 17)
 Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 Patent: US 6566127-A 2586 20-MAY-2003;
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 DB 2 TGAACCTAGGAAA 15

RESULT 5
 AX189329/c 18 bp DNA linear PAT 08-AUG-2001
 LOCUS AX189329

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 : Search time 273.308 Seconds
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Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	15	8.4	25	US-10-719-900-631977	Sequence 631977, A
C 2	15	8.4	25	US-10-719-956-616622	Sequence 616622, A
C 3	15	8.4	25	US-11-036-317-231424	Sequence 231424, A
C 4	15	8.4	25	US-11-036-317-267405	Sequence 267405, A
C 5	15	8.4	25	US-11-036-317-357375	Sequence 357375, A
C 6	15	8.4	25	US-11-036-317-365808	Sequence 365808, A
C 7	15	8.4	25	US-11-036-317-392157	Sequence 392157, A

C 8	15	8.4	25	US-11-036-317-895084	Sequence 895084, A
C 9	15	8.4	25	US-11-036-317-915102	Sequence 915102, A
C 10	15	8.4	25	US-11-036-317-972328	Sequence 972328, A
C 11	14	7.9	20	US-10-146-860-34	Sequence 34, A
C 12	14	7.9	20	US-10-272-811-41	Sequence 41, A
C 13	14	7.9	20	US-10-272-727-41	Sequence 41, A
C 14	14	7.9	21	US-10-745-377-187	Sequence 187, A
C 15	14	7.9	21	US-10-872-113-187	Sequence 187, A
C 16	14	7.9	25	US-10-098-2638-47995	Sequence 47995, A
C 17	14	7.9	25	US-10-098-2638-129956	Sequence 129956, A
C 18	14	7.9	25	US-10-719-900-224006	Sequence 224006, A
C 19	14	7.9	25	US-10-719-900-307529	Sequence 307529, A
C 20	14	7.9	25	US-10-719-900-320873	Sequence 320873, A
C 21	14	7.9	25	US-10-719-900-375276	Sequence 375276, A
C 22	14	7.9	25	US-10-719-900-394661	Sequence 394661, A
C 23	14	7.9	25	US-10-719-900-426941	Sequence 426941, A
C 24	14	7.9	25	US-10-719-900-580483	Sequence 580483, A
C 25	14	7.9	25	US-10-719-900-647614	Sequence 647614, A
C 26	14	7.9	25	US-10-719-900-670297	Sequence 670297, A
C 27	14	7.9	25	US-10-719-900-719682	Sequence 719682, A
C 28	14	7.9	25	US-10-719-900-735247	Sequence 735247, A
C 29	14	7.9	25	US-10-719-900-744322	Sequence 744322, A
C 30	14	7.9	25	US-10-719-900-800171	Sequence 800171, A
C 31	14	7.9	25	US-10-719-900-856792	Sequence 856792, A
C 32	14	7.9	25	US-10-719-900-885037	Sequence 885037, A
C 33	14	7.9	25	US-10-809-189-21863	Sequence 21863, A
C 34	14	7.9	25	US-10-956-157-26675	Sequence 26675, A
C 35	14	7.9	25	US-10-956-157-199774	Sequence 199774, A
C 36	14	7.9	25	US-10-956-157-290472	Sequence 290472, A
C 37	14	7.9	25	US-10-843-527-2390	Sequence 2390, A
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C 39	14	7.9	25	US-10-843-527-209209	Sequence 209209, A
C 40	14	7.9	25	US-10-843-527-235787	Sequence 235787, A
C 41	14	7.9	25	US-10-681-773-11304	Sequence 11304, A
C 42	14	7.9	25	US-10-681-773-32516	Sequence 32516, A
C 43	14	7.9	25	US-10-681-773-45247	Sequence 45247, A
C 44	14	7.9	25	US-10-681-773-74373	Sequence 74373, A
C 45	14	7.9	25	US-10-681-773-97404	Sequence 97404, A
C 46	14	7.9	25	US-10-719-956-72776	Sequence 72776, A
C 47	14	7.9	25	US-10-719-956-81230	Sequence 81230, A
C 48	14	7.9	25	US-10-719-956-103306	Sequence 103306, A
C 49	14	7.9	25	US-10-719-956-163732	Sequence 163732, A
C 50	14	7.9	25	US-10-719-956-196840	Sequence 196840, A
C 51	14	7.9	25	US-10-719-956-269869	Sequence 269869, A
C 52	14	7.9	25	US-10-719-956-345616	Sequence 345616, A
C 53	14	7.9	25	US-10-719-956-354423	Sequence 354423, A
C 54	14	7.9	25	US-11-036-317-120815	Sequence 120815, A
C 55	14	7.9	25	US-11-036-317-129478	Sequence 129478, A
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C 57	14	7.9	25	US-11-036-317-243418	Sequence 243418, A
C 58	14	7.9	25	US-11-036-317-243418	Sequence 243418, A
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C 60	14	7.9	25	US-11-036-317-307850	Sequence 307850, A
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C 62	14	7.9	25	US-11-036-317-356005	Sequence 356005, A
C 63	14	7.9	25	US-11-036-317-389644	Sequence 389644, A
C 64	14	7.9	25	US-11-036-317-541203	Sequence 541203, A
C 65	14	7.9	25	US-11-036-317-557520	Sequence 557520, A
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C 87 13 7.3 20 21 US-10-831-901A-29337 Sequence 29337, A
C 88 13 7.3 21 9 US-09-487-318-12 Sequence 12, Appl
C 89 13 7.3 21 15 US-10-204-085-34 Sequence 34, Appl
C 90 13 7.3 21 16 US-10-299-991-20 Sequence 20, Appl
C 91 13 7.3 21 16 US-10-299-991-21 Sequence 21, Appl
C 92 13 7.3 21 16 US-10-299-991-22 Sequence 22, Appl
C 93 13 7.3 21 17 US-10-293-965-20 Sequence 20, Appl
C 94 13 7.3 21 17 US-10-293-965-22 Sequence 22, Appl
C 95 13 7.3 21 17 US-10-293-965-22 Sequence 22, Appl
C 96 13 7.3 21 21 US-10-693-712-35 Sequence 35, Appl
C 97 13 7.3 21 21 US-10-643-775-570 Sequence 570, Appl
C 98 13 7.3 21 22 US-10-485-225-88 Sequence 88, Appl
C 99 13 7.3 21 24 US-11-070-332-20 Sequence 20, Appl
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ALIGNMENTS

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; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 631977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-631977

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; Sequence 616622, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 616622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-616622
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 231424, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-231424
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 267405, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-267405
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Best Local Similarity 100.0%; Score 15; DB 24; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 23 TGAGTATGTGACTCT 9
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US-11-036-317-357375/c
; Sequence 357375, Application US/11036317
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 ; Search time 54.6219 Seconds
(without alignments)
5332.244 Million cell updates/sec

Title: US-09-887-941B-6

Perfect score: 178
Sequence: 1 gggctcgtcgtgaatgcat.....actctgcacccatttctcg 178

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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17	12	6.7	17	3	US-09-383-316-88
18	12	6.7	17	4	US-09-404-912-619
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23	12	6.7	19	4	US-09-696-791-393
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57	12	6.7	28	3	US-09-479-729B-8
58	12	6.7	28	3	US-09-261
59	12	6.7	28	3	US-09-717-209-8
60	12	6.7	31	1	US-08-136-993-19
61	12	6.7	31	2	US-08-454-557C-63
62	12	6.7	31	2	US-08-340-426D-63
63	12	6.7	31	2	US-08-450-673C-63
64	12	6.7	31	2	US-08-387-659-20
65	12	6.7	31	5	US-09-641-259B-20
66	12	6.7	31	5	PCT-US95-17111A-63
67	12	6.7	32	4	US-09-153-447-16
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69	12	6.7	32	4	US-09-721-908-54
70	12	6.7	32	1	US-08-136-993-18
71	12	6.7	41	3	US-09-066-597-14
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76	12	6.7	42	4	US-08-892-864A-23
77	12	6.7	46	3	US-09-066-597-12
78	12	6.7	47	3	US-09-641-638-671
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83	12	6.7	47	4	US-10-170-097-779
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87	12	6.7	50	3	US-08-521-872-35
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92	12	6.7	50	4	US-10-242-549-31
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94	12	6.7	50	4	US-08-704-744-10
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ALIGNMENTS

RESULT 1
US-09-396-196G-21863

Sequence 21863, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21863
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-21863

Query Match 7.9%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 TTCACGAGGGAACC 90
DB 1 TTCACGAGGGAACC 14

RESULT 2

US-08-761-243C-1
Sequence 1, Application US/08761243C

Patent No. 5879879
GENERAL INFORMATION:
APPLICANT: Kamal D. Mehta
TITLE OF INVENTION: No. 5879879e1 Cis-Acting Element In The Human LDL Receptor Pro
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,243C
FILING DATE: December 6, 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: No
HYPOTHETICAL: No
ANTI-SENSE: NO
ORIGINAL SOURCE:
US-08-761-243C-1

Query Match 7.3%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 TCACGGTTAAAA 66
DB 6 TCACGGTTAAAA 18

RESULT 3

US-08-444-818-775/C
Sequence 775, Application US/08444818

Patent No. 615087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutler, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hardin, Alisha A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 359-3876
TELEFAX: (508) 359-3885
INFORMATION FOR SEQ ID NO: 775:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer sscsh20A - derived
DESCRIPTION: from clone 5h"
US-08-444-818-775

Query Match 7.3%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 TGACTGTGTACC 169
DB 20 TGACTGTGTACC 8

RESULT 4

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 1238.07 Seconds
(without alignments)
5472.564 Million cell updates/sec

Title: US-09-887-941B-6

Perfect score: 178
Sequence: 1 gggtcgcgtcgtgcatgatc.....actctgcaccattctctg 178

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	13	7.3	25 7	H93534 yv08g12.r1
2	13	7.3	33 8	BH758806 SALK_0313
3	13	7.3	35 7	N38850 yv08e11.r1
4	13	7.3	40 8	AZ575761 AST-T32B0
5	13	7.3	42 8	BH000535 2M0288B05
6	13	7.3	46 7	R24341 y932h04.r1
7	13	7.3	46 7	R36760 y922a04.r1
8	13	7.3	49 6	C20874 HUMG000494
9	13	7.3	50 1	AU104332 AU104332
10	13	7.3	31 1	AA61514 y034h05.r
11	12	6.7	34 7	T89869 yd99e12.r1
12	12	6.7	34 8	AZ511608 1M0356A13
13	12	6.7	35 4	AI801185 t079h04.x
14	12	6.7	35 8	AZ658296 1M0535F04
15	12	6.7	36 7	R85453 yq26g04.r1
16	12	6.7	38 1	AI088003 co24h05.x
17	12	6.7	38 7	H45829 y081b05.r1
18	12	6.7	38 9	BX658508 Arabidops
19	12	6.7	40 7	W96297 ze42a10.r1
20	12	6.7	41 1	AA019796 ze62h02.r
21	12	6.7	43 6	CB471442 an39.A03
22	12	6.7	43 7	H59371 y127h06.r1
23	12	6.7	43 7	R07988 yf16f09.r1
24	12	6.7	43 8	BH805136 1008065F0

25	12	6.7	43 9	BX651282 Arabidops
26	12	6.7	43 1	CL528416 ASV10D06
27	12	6.7	44 1	AI494250 qy98a01.x
28	12	6.7	45 7	N79952 yz86g01.r1
29	12	6.7	47 9	BX244624 Dario rer
30	12	6.7	48 8	AZ336853 1M0067K15
31	12	6.7	49 5	BQ587334 E012340w-
32	12	6.7	49 5	BQ587334 E012340w-
33	12	6.7	49 7	D11989 HUM0005134
34	12	6.7	50 1	AU102898 AU102898
35	12	6.7	50 1	AU106860 AU106860
36	12	6.7	50 1	AU106864 AU106864
37	12	6.7	50 1	AU106865 AU106865
38	12	6.7	50 8	AZ575772 AST-T32B0
39	12	6.7	50 9	BX894616 Arabidops
40	12	6.2	20 9	AG195490 Pan trog1
41	12	6.2	22 9	AG201938 Pan trog1
42	12	6.2	24 8	AZ491197 1M0324C10
43	12	6.2	25 8	AZ486309 1M0314B18
44	12	6.2	25 8	AZ586862 1M0394A10
45	12	6.2	25 8	AZ307056 1M0008Q23
46	12	6.2	26 8	AZ806070 2M0067Q21
47	12	6.2	29 8	AZ619274 1M0451J02
48	12	6.2	29 9	AG018559 Homo sapi
49	12	6.2	30 8	AZ408503 1M0179P12
50	12	6.2	30 8	AZ633504 1M0488K13
51	12	6.2	30 8	BZ352917 SALK_1194
52	12	6.2	31 4	BG503651 602549510
53	12	6.2	31 9	DR34P19S Dario rer
54	12	6.2	32 1	AJ666396 Arabidops
55	12	6.2	32 2	BE318502 NF071E02L
56	12	6.2	32 2	BE318791 NF075H02L
57	12	6.2	32 8	AZ946018 2M0207D07
58	12	6.2	34 1v	AU014066 AU014066
59	12	6.2	34 1	AU248882 AU248882
60	12	6.2	34 7	U44145 ENU44145 AS
61	12	6.2	34 9	AG201685 Pan trog1
62	12	6.2	35 8	AZ583415 1M0378024
63	12	6.2	35 8	AZ815423 2M0083H09
64	12	6.2	36 9	AJ594687 Arabidops
65	12	6.2	37 8	BZ770609 SALK_1435
66	12	6.2	37 8	CC057412 SALK_1417
67	12	6.2	38 2	BF507311 BFO507311 8949F-20
68	12	6.2	38 8	BZ287177 SALK_0205
69	12	6.2	38 9	CNS07FKF Alphelais
70	12	6.2	38 9	HSMC39C10 X88090 H.sapiens D
71	12	6.2	40 1	AI495995 sa94c05.y
72	12	6.2	40 9	AL950398 Arabidops
73	12	6.2	41 2	AM246496 Arabidops
74	12	6.2	41 8	AZ412970 1M0186G15
75	12	6.2	42 1	AA703076 2176h06.s
76	12	6.2	42 2	AV952678 AV952678
77	12	6.2	42 7	D19560 MUGS00962
78	12	6.2	43 1	AA625513 af72e05.r
79	12	6.2	43 3	R52204 y985f06.r1
80	12	6.2	43 7	BZ289075 SALK_0224
81	12	6.2	44 2	AV958656 AV958656
82	12	6.2	44 8	AZ403273 1M0171G12
83	12	6.2	45 9	BX243596 Dario rer
84	12	6.2	45 9	BX243596 Dario rer
85	12	6.2	46 8	AZ820550 2M0092M18
86	12	6.2	46 9	CI868623 EY14285-5
87	12	6.2	47 1	AV947917 AV947917
88	12	6.2	47 4	BU000922 BU000922
89	12	6.2	47 8	BZ597134 SALK_0994
90	12	6.2	48 2	AV958077 AV958077
91	12	6.2	48 9	AV947788 AV947788
92	12	6.2	49 1	AW733869 AW733869
93	12	6.2	49 9	CC325445 TEA127 Ba
94	12	6.2	49 9	AG191198 Pan trog1
95	12	6.2	50 1	AU102624 AU102624
96	12	6.2	50 1	AU102625 AU102625
97	12	6.2	50 1	AU102626 AU102626

C 98 11 6.2 50 1 AU02674 AU02674
C 99 11 6.2 50 1 AU02677 AU02677
C 100 11 6.2 50 1 AU05599 AU05599

ALIGNMENTS

RESULT 1
LOCUS H93534 25 bp mRNA linear EST 01-DEC-1995

DEFINITION Y08912.1 Soares fetal liver spleen INFES Homo sapiens CDNA clone IMAGE:242182 5' similar to gb|U87933|HUMALU364 Human carcinoma cell-derived Alu RNA transcript, (rRNA);, mRNA sequence.

ACCESSION H93534.1 GI:1099862

VERSION H93534.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 25)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1. 25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3791315"

/db_xref="taxon:9606"

/clone="IMAGE:242182"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen INFES"

/note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with 5' Pac I - oligo(dT) primer 15' AACTGGAAGAAATTATTAACATCTTTTCTTTTCTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.3%; Score 13; DB 7; Length 25;

Best Local Similarity 100.0%; Pred. No. 5.1e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 159 ACTGTGACCA 171

DB 1 ACTGTGACCA 13

RESULT 2
LOCUS BH758806/c 33 bp DNA linear GSS 01-MAR-2002

DEFINITION SALX_031345.51.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALX_031345.51.20.x, genomic survey sequence.

ACCESSION BH758806.1 GI:19044689

VERSION BH758806

KEYWORDS GSS.

ORGANISM Arabidopsis thaliana (thale cress)

DEFINITION Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 33)

AUTHORS Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrihab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

COMMENT Contact: Joseph R. Ecker

The Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g53700.

Class: TDNA tagged.

Location/Qualifiers

1. 33

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALX_031345.51.20.x"

/note="TPCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 7.3%; Score 13; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 5.1e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 57 CGGCTTAACCC 69

DB 27 CGGCTTAACCC 15

RESULT 3

LOCUS N38850/c

DEFINITION

N38850 35 bp mRNA linear EST 19-JAN-1996

Y80811.1 Soares multiple sclerosis 2BHSMP Homo sapiens CDNA

clone IMAGE:279884 5' similar to gb|U87933|HUMALU364 Human

carcinoma cell-derived Alu RNA transcript, (rRNA); gb:M96956

EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN);, mRNA

sequence.

ACCESSION N38850

VERSION N38850.1 GI:1162057

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 35)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 187.181 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941b-6

Perfect score: 178
Sequence: 1 99gtcgcgtcgtcgaatgcac.....actctgcaccattctctg 178

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004as:*\n13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	8.4	35	3	AAC64260 Soybean c
C 2	14	7.9	20	12	AD115588 Human c
C 3	14	7.9	20	12	ADM34135 Human c
C 4	14	7.9	20	12	ADM11332 Human c
C 5	14	7.9	21	4	AAF93016 Wild type
C 6	14	7.9	25	9	ACT48004 Human m/c
C 7	14	7.9	25	9	ACK29975 Human m/c
C 8	14	7.9	26	10	ADCS4012 SAM4 PCR
C 9	14	7.9	41	6	AB244347 Human ATP
C 10	14	7.9	41	6	AB246696 Human ATP
C 11	14	7.9	42	2	AAT25575 Human gen
C 12	13	7.3	17	12	ADP09407 Extend pr
C 13	13	7.3	18	12	AD081024 Human p/r
C 14	13	7.3	19	12	ADM6491 Human sh
C 15	13	7.3	19	12	ADP09402 Extend pr
C 16	13	7.3	19	12	ADP26951 Human P-C
C 17	13	7.3	20	8	AA118844 FPI enhan
C 18	13	7.3	20	8	ACC55324 Human ADA
C 19	13	7.3	20	12	ADH70943 Human Vde
C 20	13	7.3	20	13	ADT01088 Novel mut

C 21	13	7.3	21	2	AA061954 Human tYP
C 22	13	7.3	21	3	AA089981 PCR prime
C 23	13	7.3	21	4	AA017802 Zea may
C 24	13	7.3	21	8	AB221583 Biliary g
C 25	13	7.3	21	9	ADB81017 RING-SH c
C 26	13	7.3	21	9	ADB81016 RING-SH c
C 27	13	7.3	21	9	ADB81018 RING-SH c
C 28	13	7.3	21	10	ADD19935 Oreochrom
C 29	13	7.3	21	10	AA156250 Human ubi
C 30	13	7.3	21	10	AA156249 Human ubi
C 31	13	7.3	21	10	AA156248 Human ubi
C 32	13	7.3	21	10	ADH73577 siRNA POS
C 33	13	7.3	21	10	ADH73575 siRNA POS
C 34	13	7.3	21	13	ADR89709 Human POS
C 35	13	7.3	21	13	ADR89710 Human POS
C 36	13	7.3	21	13	ADR89708 Human POS
C 37	13	7.3	21	13	ADS34641 POSH prot
C 38	13	7.3	21	13	ADS34640 POSH prot
C 39	13	7.3	21	13	ADS34642 POSH prot
C 40	13	7.3	22	8	ABX56408 Human NOV
C 41	13	7.3	22	10	ADH73576 siRNA POS
C 42	13	7.3	22	12	AD016814 4 synthet
C 43	13	7.3	24	4	AAH48127 Ribonucle
C 44	13	7.3	24	4	AA165251 Human diH
C 45	13	7.3	24	4	AAH75870 Human rev
C 46	13	7.3	24	5	AAH44468 Enolpyruv
C 47	13	7.3	24	5	AA168386 Human ATP
C 48	13	7.3	24	6	AA166326 Human tHy
C 49	13	7.3	24	6	ABQ75907 Human L1
C 50	13	7.3	24	6	ABK86233 Arginyl t
C 51	13	7.3	25	9	ACT103920 Human m/c
C 52	13	7.3	25	9	ACT113157 Human m/c
C 53	13	7.3	25	9	ACK05705 Human m/c
C 54	13	7.3	25	9	ACT131980 Human m/c
C 55	13	7.3	25	9	ACT187917 Human m/c
C 56	13	7.3	25	9	ACT190803 Human m/c
C 57	13	7.3	25	9	ACK07676 Human m/c
C 58	13	7.3	25	9	ACK05340 Human m/c
C 59	13	7.3	25	9	ACT182151 Human m/c
C 60	13	7.3	26	12	ADP30756 Bacillus
C 61	13	7.3	28	2	AA118861 Human low
C 62	13	7.3	29	2	AAQ94508 Human/mur
C 63	13	7.3	29	2	AAT18622 Chimaeric
C 64	13	7.3	30	4	AA017808 Zea may
C 65	13	7.3	30	5	AB139683 Human cub
C 66	13	7.3	31	5	AA160078 Primer #2
C 67	13	7.3	33	6	ABA96568 Human tYr
C 68	13	7.3	33	6	ABA95478 Human diH
C 69	13	7.3	33	10	AA156444 Primer 3
C 70	13	7.3	37	10	ADG79070 Schizophr
C 71	13	7.3	39	2	AA669917 M. tuberc
C 72	13	7.3	39	3	AA027506 M13-tagge
C 73	13	7.3	41	6	ABA96570 Human tYr
C 74	13	7.3	41	6	ABA96571 Human tYr
C 75	13	7.3	41	6	ABN68870 Human mac
C 76	13	7.3	41	6	ABN68871 Human mac
C 77	13	7.3	41	6	ABZ47452 Human ATP
C 78	13	7.3	41	6	ABZ47536 Human ATP
C 79	13	7.3	41	6	ABZ47125 Human ATP
C 80	13	7.3	41	6	ABZ43249 Human ATP
C 81	13	7.3	41	6	ABA95480 Human diH
C 82	13	7.3	41	6	ABA95481 Human diH
C 83	13	7.3	41	10	AA156446 Probe 1 r
C 84	13	7.3	41	12	ADK17858 Cytochrom
C 85	13	7.3	47	3	AA267325 Human map
C 86	13	7.3	47	13	ADR35380 Human n/c
C 87	13	7.3	47	13	ADR35379 Human n/c
C 88	13	7.3	47	13	ADR35398 Human n/c
C 89	13	7.3	47	13	ADR35399 Human n/c
C 90	13	7.3	49	8	ABZ09708 Human oli
C 91	13	7.3	49	10	ABZ79161 Tumour su
C 92	13	7.3	50	6	ABZ07763 Human leu
C 93	12	6.7	13	5	ABF99107 Oligonuc1

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c 94 12 6.7 13 5 ABC96633 Abc96633 Oligonuc1
95 12 6.7 13 5 ABP99106 Abf99106 Oligonuc1
96 12 6.7 13 5 ABC96632 Abc96632 Oligonuc1
97 12 6.7 14 8 Aca61142 Aca61142 Adaptein
98 12 6.7 15 2 Aat52086 Aat52086 Human ICA
99 12 6.7 17 3 Aaa36560 Aaa36560 Human gen
c 100 12 6.7 17 3 Aaa87041 Aaa87041 Probe to
```

ALIGNMENTS

RESULT 1

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AC64260/c
ID AAC64260 standard; DNA; 35 BP.
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XX AAC64260;
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DT 23-FEB-2001 (first entry)
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DE Soybean cotyledon leucine aminopeptidase (LAP) PCR primer, SEQ ID NO:9.
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KW Soybean cotyledon; leucine aminopeptidase; LAP; recombinant production;
```

```
KM plasmid construction; PCR primer; ss.
```

```
XX Glycine max.
```

```
PN JP2000262286-A.
```

```
PD 26-SEP-2000.
```

```
PF 15-MAR-1999; 99JP-00068353.
```

```
PR 15-MAR-1999; 99JP-00068353.
```

```
XX (AJIN ) AJINOMOTO KK.
```

```
DR WPI; 2000-682117/67.
```

```
PT Novel DNA encoding leucine aminopeptidase useful for the recombinant
```

```
PT preparation of leucine aminopeptidase.
```

```
PS Example 3; Page 20; 22pp; Japanese.
```

```
XX The invention relates to a soybean leucine aminopeptidase (AAB29636), and
```

```
CC CDNA encoding it (AAC64260), derived from cotyledon tissue. The invention
```

```
CC also relates to variants of soybean cotyledon LAP which retain activity,
```

```
CC recombinant vectors and host cells comprising DNA encoding the soybean
```

```
CC cotyledon LAP, and a method for the recombinant production of the LAP.
```

```
CC The method of the invention can be used for the large scale recombinant
```

```
CC preparation of soybean cotyledon leucine aminopeptidase. The present
```

```
CC sequence represents a soybean cotyledon leucine aminopeptidase PCR primer
```

```
CC used in plasmid construction in an exemplification of the invention
```

```
XX SEQ Sequence 35 BP; 7 A; 8 C; 10 G; 10 T; 0 U; 0 Other;
```

```
OY Query Match 8.4%; Score 15; DB 3; Length 35;
```

```
XX Best Local Similarity 100.0%; Pred. No. 7e+02;
```

```
AC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
DT 22-APR-2004 (first entry)
```

```
XX
```

```
DE Human phosphodiesterase 4D antisense oligonucleotide #14.
```

```
XX cytosolic; cardiant; antiinflammatory; antimicrobial; antisense therapy;
```

```
KW phosphodiesterase inhibitor 4D; phosphodiesterase 4D; cancer;
```

```
KM cardiovascular disease; inflammation; infection; inflammation;
```

```
XX tumour formation; antisense technology; human; ss.
```

```
OS Homo sapiens.
```

```
XX Key Location/Qualifiers
```

```
FT modified_base 1..20
```

```
FT /tag= b
```

```
FT /mod_base= OTHER
```

```
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
```

```
FT are 5-methylcytidines"
```

```
FT modified_base 1..5
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```
FT /tag= a
```

```
FT /mod_base= OTHER
```

```
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
```

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FT modified_base 15..20
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FT /tag= c
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```
FT /mod_base= OTHER
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FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
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```
XX US2003220273-A1.
```

```
XX 27-NOV-2003.
```

```
XX 15-MAY-2002; 2002US-00146860.
```

```
XX 15-MAY-2002; 2002US-00146860.
```

```
XX (ISIS-) ISIS PHARM INC.
```

```
XX Bennett CF, Dobie KW, Roach MP;
```

```
XX WPI; 2004-060214/06.
```

```
XX New antisense compounds targeted to nucleic acid molecules encoding
```

```
XX phosphodiesterase 4D, useful for treating diseases associated with
```

```
XX expression of phosphodiesterase 4D, e.g. cancer, cardiovascular disease
```

```
XX or inflammation.
```

```
XX Example 15; SEQ ID NO 34; 72pp; English.
```

```
XX The invention describes a compound 8-80 nucleobases in length targeted to
```

```
XX a nucleic acid molecule encoding phosphodiesterase 4D. The compound
```

```
XX specifically hybridises with the nucleic acid molecule encoding
```

```
XX phosphodiesterase 4D and inhibits the expression of phosphodiesterase 4D,
```

```
XX or specifically hybridises with at least an 8-nucleobase portion of an
```

```
XX active site on a nucleic acid molecule encoding phosphodiesterase 4D. The
```

```
XX antisense oligonucleotides and compounds are useful for modulating the
```

```
XX expression of phosphodiesterase 4D, and for treating diseases or
```

```
XX conditions associated with expression of phosphodiesterase 4D, e.g.
```

```
XX cancer, cardiovascular disease or inflammation. The antisense compounds
```

```
XX are also useful as research reagents and kits, or in diagnostic,
```

```
XX therapeutic and prophylaxis applications, e.g. to prevent or delay
```

```
XX infection, inflammation or tumour formation. This sequence represents a
```

```
XX human phosphodiesterase 4D antisense oligonucleotide.
```

```
XX SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
```

```
OY Query Match 7.9%; Score 14; DB 12; Length 20;
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XX Best Local Similarity 100.0%; Pred. No. 2.5e+03;
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AC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 81 CGAGGGAACACGCT 94
```

```
XX |||||
```

```
DB 15 CGAGGGAACACGCT 2
```

```
XX |||||
```

```
AC
```

```
DT
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XX
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XX
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XX
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Tue Oct 11 10:02:34 2005

us-09-887-941b-6.olig_sz50.rge

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1092.17 Seconds
(without alignments)
7897.122 Million cell updates/sec

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Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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12: gb_sy:1
13: gb_un:1
14: gb_vi:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	13	7.3	18	6	CQ788001	CQ788001 Sequence
C 3	13	7.3	19	6	CQ824199	CQ824199 Sequence
C 4	13	7.3	20	6	AR118841	AR118841 Sequence
C 5	13	7.3	20	6	IO6413	IO6413 Sequence 33
C 6	13	7.3	20	12	AB069586	AB069586 Synthetic
C 7	13	7.3	21	6	AR074287	AR074287 Sequence
C 8	13	7.3	21	6	BD182298	BD182298 Stem cell
C 9	13	7.3	21	6	BD243279	BD243279 Human liv
C 10	13	7.3	21	6	AX032649	AX032649 Sequence
C 11	13	7.3	21	6	AX235821	AX235821 Sequence
C 12	13	7.3	21	6	AX776612	AX776612 Sequence
C 13	13	7.3	21	6	AX804402	AX804402 Sequence
C 14	13	7.3	22	6	AR308944	AR308944 Sequence
C 15	13	7.3	22	6	AR317075	AR317075 Sequence
C 16	13	7.3	22	6	AX776611	AX776611 Sequence
C 17	13	7.3	26	6	AX951882	AX951882 Sequence
C 18	13	7.3	26	6	AX253564	AX253564 Sequence
C 19	13	7.3	29	6	AX253564	AX253564 Sequence

C 20	13	7.3	30	6	BD187806	BD187806 Novel pol
C 21	13	7.3	30	6	AX235827	AX235827 Sequence
C 22	13	7.3	30	6	BD105529	BD105529 Novel pol
C 23	13	7.3	31	6	AR448492	AR448492 Sequence
C 24	13	7.3	31	6	AX078478	AX078478 Sequence
C 25	13	7.3	31	6	AX08601	AX08601 Oligonucleo
C 26	13	7.3	33	6	AR337935	AR337935 Sequence
C 27	13	7.3	34	6	AR118842	AR118842 Sequence
C 28	13	7.3	34	6	IO6414	IO6414 Sequence 34
C 29	13	7.3	39	6	AX022689	AX022689 Sequence
C 30	13	7.3	41	6	AX513835	AX513835 Sequence
C 31	13	7.3	41	6	AX517711	AX517711 Sequence
C 32	13	7.3	41	6	AX518142	AX518142 Sequence
C 33	13	7.3	47	6	AR289937	AR289937 Sequence
C 34	13	7.3	49	6	AX523198	AX523198 Sequence
C 35	12	6.7	15	6	AR056132	AR056132 Sequence
C 36	12	6.7	15	6	AR113890	AR113890 Sequence
C 37	12	6.7	15	6	AR633147	AR633147 Sequence
C 38	12	6.7	17	6	AR153250	AR153250 Sequence
C 39	12	6.7	17	6	BD241672	BD241672 Methods a
C 40	12	6.7	17	6	AR210968	AR210968 Sequence
C 41	12	6.7	17	6	AR483173	AR483173 Sequence
C 42	12	6.7	17	6	AR533227	AR533227 Sequence
C 43	12	6.7	17	6	AR367785	AR367785 Sequence
C 44	12	6.7	18	6	AR367785	AR367785 Sequence
C 45	12	6.7	19	6	AR233457	AR233457 Sequence
C 46	12	6.7	19	6	AX226153	AX226153 Sequence
C 47	12	6.7	19	6	AX709267	AX709267 Sequence
C 48	12	6.7	19	6	AX709268	AX709268 Sequence
C 49	12	6.7	19	6	AR233789	AR233789 Sequence
C 50	12	6.7	20	6	AX292942	AX292942 Sequence
C 51	12	6.7	20	6	CQ796783	CQ796783 Sequence
C 52	12	6.7	21	6	AR182144	AR182144 Sequence
C 53	12	6.7	21	6	AR533898	AR533898 Sequence
C 54	12	6.7	21	6	AR633708	AR633708 Sequence
C 55	12	6.7	21	6	AX147852	AX147852 Sequence
C 56	12	6.7	22	6	AX521901	AX521901 Sequence
C 57	12	6.7	22	6	AX674899	AX674899 Sequence
C 58	12	6.7	22	6	AX798208	AX798208 Sequence
C 59	12	6.7	24	6	CQ788012	CQ788012 Sequence
C 60	12	6.7	24	6	CQ875604	CQ875604 Sequence
C 61	12	6.7	24	6	AX18867	AX18867 Sequence
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C 64	12	6.7	24	6	AX798208	AX798208 Sequence
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C 68	12	6.7	25	6	AR240239	AR240239 Sequence
C 69	12	6.7	25	6	AR488670	AR488670 Sequence
C 70	12	6.7	26	6	AX110770	AX110770 Sequence
C 71	12	6.7	26	6	BD273260	BD273260 Methods f
C 72	12	6.7	27	6	BD273261	BD273261 Methods f
C 73	12	6.7	27	6	AX224542	AX224542 Sequence
C 74	12	6.7	27	6	AX299936	AX299936 Sequence
C 75	12	6.7	27	6	AX480648	AX480648 Sequence
C 76	12	6.7	27	6	AX616734	AX616734 Sequence
C 77	12	6.7	27	6	AR142426	AR142426 Sequence
C 78	12	6.7	28	6	AR232961	AR232961 Sequence
C 79	12	6.7	28	6	AR447128	AR447128 Sequence
C 80	12	6.7	29	6	AX183709	AX183709 Sequence
C 81	12	6.7	29	6	AX686106	AX686106 Sequence
C 82	12	6.7	30	6	IO5530	IO5530 Sequence 17
C 83	12	6.7	30	6	AX793616	AX793616 Sequence
C 84	12	6.7	30	10	MM41104	MM41104 Sequence
C 85	12	6.7	31	6	AR051493	AR051493 Sequence
C 86	12	6.7	31	6	AR072633	AR072633 Sequence
C 87	12	6.7	31	6	AR073178	AR073178 Sequence
C 88	12	6.7	31	6	BD274933	BD274933 DNA ENCOD
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C 90	12	6.7	31	6	E18849	E18849 Primer. 4/1
C 91	12	6.7	31	6	E12075	E12075 Sequence 19
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c 93 12 6.7 31 6 AR240233 Sequence
 94 12 6.7 32 6 AR390458 Sequence
 95 12 6.7 32 6 AR390464 Sequence
 96 12 6.7 32 6 AR478854 Sequence
 97 12 6.7 32 6 AX203795 Sequence
 98 12 6.7 35 6 112074
 99 12 6.7 40 6 BD180823
 c 100 12 6.7 40 6 AX099972
 AR240233 Sequence
 AR390458 Sequence
 AR390464 Sequence
 AR478854 Sequence
 AX203795 Sequence
 112074 Sequence
 BD180823 Array of
 AX099972 Sequence

ALIGNMENTS

RESULT 1
 AX092775/c
 LOCUS AX092775 21 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 187 from Patent WO0115676.
 ACCESSION AX092775 GI:13444832
 VERSION AX092775.1 GI:13444832
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
 Compositions and methods for modulating hdl cholesterol and
 triglyceride levels
 Patent: WO 0115676-A 187 08-MAR-2001;
 University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
 Location/Qualifiers
 1..21
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

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QY 61 TTTAAACCCGACCA 74
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 17 TTTAAACCCGACCA 4

RESULT 2
 CQ788001/c
 LOCUS CQ788001 18 bp DNA linear PAT 24-MAR-2004
 DEFINITION Sequence 307 from Patent WO2004020664.
 ACCESSION CQ788001
 VERSION CQ788001.1 GI:45722959
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE
 1 Geldermann, H., Preuss, S. and Han, Y.
 Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
 Patent: WO 2004020664-A 307 11-MAR-2004;
 Universitaet Hohenheim (DE)
 Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="R ckw its-Primer f r M10"

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QY 159 ACTCTGTACCCA 171
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 16 ACTCTGTACCCA 4

RESULT 3
 CQ824199/c
 LOCUS CQ824199 19 bp DNA linear PAT 21-JUN-2004
 DEFINITION Sequence 52 from Patent EP1428893.
 ACCESSION CQ824199
 VERSION CQ824199.1 GI:49021151
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE
 1 Sprecher, E. and Bergman, R.
 Methods of and compositions for modulating hair growth via
 p-cadherin modulators
 Patent: EP 1428893-A 52 16-JUN-2004;
 Sprecher, Eli (IL); Bergman, Reuven (IL)
 Location/Qualifiers
 1..19
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic oligonucleotide"

ORIGIN

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QY 159 ACTCTGTACCCA 171
 |||||
 14 ACTCTGTACCCA 2

RESULT 4
 AR118841/c
 LOCUS AR118841 20 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 775 from patent US 6150087.
 ACCESSION AR118841
 VERSION AR118841.1 GI:14100751
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 20)
 AUTHORS Chen, D.Y.
 TITLE NABV diagnostics and vaccines
 JOURNAL Patent: US 6150087-A 775 21-NOV-2000;
 Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

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Query Match 7.3%; Score 13; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 TGACTCTGTACCC 169
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 20 TGACTCTGTACCC 8

RESULT 5
 I06413/c
 LOCUS I06413 20 bp DNA linear PAT 02-DEC-1994
 DEFINITION Sequence 33 from Patent EP 0318216.
 ACCESSION I06413

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 ; Search time 589.607 Seconds
(without alignments)
4536.068 Million cell updates/sec

Title: US-09-887-941B-5

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SUMMARIES

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C 4	16	4.2	25	21	US-10-719-900-362302
C 5	16	4.2	25	21	US-10-809-189-25049
C 6	16	4.2	25	22	US-10-719-956-258472
C 7	16	4.2	25	24	US-11-036-317-253623

C 8	16	4.2	25	24	US-11-036-317-322487	Sequence 322487,
C 9	16	4.2	25	24	US-11-036-317-330735	Sequence 330735,
C 10	16	4.2	25	24	US-11-036-317-405052	Sequence 405052,
C 11	16	4.2	25	24	US-11-036-317-615228	Sequence 615228,
C 12	15	3.9	25	24	US-10-098-263B-13527	Sequence 13527, A
C 13	15	3.9	25	15	US-10-098-263B-14976	Sequence 14976, A
C 14	15	3.9	25	15	US-10-098-263B-56485	Sequence 56485, A
C 15	15	3.9	25	15	US-10-098-263B-92176	Sequence 92176, A
C 16	15	3.9	25	15	US-10-098-263B-102608	Sequence 102608,
C 17	15	3.9	25	15	US-10-098-263B-117353	Sequence 117353,
C 18	15	3.9	25	21	US-10-719-900-184755	Sequence 184755,
C 19	15	3.9	25	21	US-10-719-900-274055	Sequence 274055,
C 20	15	3.9	25	21	US-10-719-900-294631	Sequence 294631,
C 21	15	3.9	25	21	US-10-719-900-485832	Sequence 485832,
C 22	15	3.9	25	21	US-10-719-900-717793	Sequence 717793,
C 23	15	3.9	25	21	US-10-719-900-873588	Sequence 873588,
C 24	15	3.9	25	21	US-10-719-900-978474	Sequence 978474,
C 25	15	3.9	25	21	US-10-956-157-40197	Sequence 40197, A
C 26	15	3.9	25	21	US-10-956-157-40198	Sequence 40198, A
C 27	15	3.9	25	21	US-10-956-157-40199	Sequence 40199, A
C 28	15	3.9	25	21	US-10-956-157-40204	Sequence 40204, A
C 29	15	3.9	25	21	US-10-956-157-40208	Sequence 40208, A
C 30	15	3.9	25	21	US-10-956-157-143285	Sequence 143285,
C 31	15	3.9	25	21	US-10-956-157-263877	Sequence 263877,
C 32	15	3.9	25	22	US-10-719-956-5686	Sequence 5686, Ap
C 33	15	3.9	25	22	US-10-719-956-428112	Sequence 428112,
C 34	15	3.9	25	22	US-10-719-956-446988	Sequence 446988,
C 35	15	3.9	25	22	US-10-719-956-476562	Sequence 476562,
C 36	15	3.9	25	22	US-10-719-956-635154	Sequence 635154,
C 37	15	3.9	25	24	US-11-036-317-150536	Sequence 150536,
C 38	15	3.9	25	24	US-11-036-317-297949	Sequence 297949,
C 39	15	3.9	25	24	US-11-036-317-335532	Sequence 335532,
C 40	15	3.9	25	24	US-11-036-317-337172	Sequence 337172,
C 41	15	3.9	25	24	US-11-036-317-441249	Sequence 441249,
C 42	15	3.9	25	24	US-11-036-317-504721	Sequence 504721,
C 43	15	3.9	25	24	US-11-036-317-590629	Sequence 590629,
C 44	15	3.9	25	24	US-11-036-317-682570	Sequence 682570,
C 45	15	3.9	25	24	US-11-036-317-777030	Sequence 777030,
C 46	15	3.9	25	24	US-11-036-317-832982	Sequence 832982,
C 47	15	3.9	25	24	US-11-036-317-854966	Sequence 854966,
C 48	15	3.9	25	24	US-11-036-317-955867	Sequence 955867,
C 49	15	3.9	25	24	US-10-319-908-82	Sequence 82,
C 50	15	3.9	25	19	US-10-786-720-3488	Sequence 3488, Ap
C 51	14	3.6	21	19	US-10-786-720-3489	Sequence 3489, Ap
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C 53	14	3.6	21	19	US-10-786-720-4190	Sequence 4190, Ap
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C 55	14	3.6	21	19	US-10-786-720-4927	Sequence 4927, Ap
C 56	14	3.6	21	19	US-10-786-720-4928	Sequence 4928, Ap
C 57	14	3.6	21	19	US-10-786-720-4929	Sequence 4929, Ap
C 58	14	3.6	21	19	US-10-751-736-7339	Sequence 7339, Ap
C 59	14	3.6	21	17	US-10-450-875-12	Sequence 12, App
C 60	14	3.6	25	15	US-10-098-263B-22057	Sequence 22057, A
C 61	14	3.6	25	21	US-10-719-900-17086	Sequence 17086, A
C 62	14	3.6	25	21	US-10-719-900-86662	Sequence 86662, A
C 63	14	3.6	25	21	US-10-719-900-99180	Sequence 99180, A
C 64	14	3.6	25	21	US-10-719-900-101759	Sequence 101759,
C 65	14	3.6	25	21	US-10-719-900-142210	Sequence 142210,
C 66	14	3.6	25	21	US-10-719-900-153476	Sequence 153476,
C 67	14	3.6	25	21	US-10-719-900-158422	Sequence 158422,
C 68	14	3.6	25	21	US-10-719-900-170925	Sequence 170925,
C 69	14	3.6	25	21	US-10-719-900-171334	Sequence 171334,
C 70	14	3.6	25	21	US-10-719-900-178054	Sequence 178054,
C 71	14	3.6	25	21	US-10-719-900-216680	Sequence 216680,
C 72	14	3.6	25	21	US-10-719-900-255802	Sequence 255802,
C 73	14	3.6	25	21	US-10-719-900-373190	Sequence 373190,
C 74	14	3.6	25	21	US-10-719-900-398044	Sequence 398044,

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c 83 14 3.6 25 21 US-10-719-900-645541, Sequence 645541,
c 84 14 3.6 25 21 US-10-719-900-734326, Sequence 734326,
c 85 14 3.6 25 21 US-10-719-900-734809, Sequence 734809,
c 86 14 3.6 25 21 US-10-719-900-759011, Sequence 759011,
c 87 14 3.6 25 21 US-10-719-900-789234, Sequence 789234,
c 88 14 3.6 25 21 US-10-719-900-897876, Sequence 897876,
c 89 14 3.6 25 21 US-10-719-900-932580, Sequence 932580,
c 90 14 3.6 25 21 US-10-719-900-955656, Sequence 955656,
c 91 14 3.6 25 21 US-10-809-189-2879, Sequence 2879, Ap
c 92 14 3.6 25 21 US-10-809-189-643929, Sequence 643929, A
c 93 14 3.6 25 21 US-10-809-189-643929, Sequence 643929, A
c 94 14 3.6 25 21 US-10-809-189-117483, Sequence 117483,
c 95 14 3.6 25 21 US-10-956-157-40203, Sequence 40203, A
c 96 14 3.6 25 21 US-10-956-157-173490, Sequence 173490,
c 97 14 3.6 25 21 US-10-956-157-271920, Sequence 271920,
c 98 14 3.6 25 22 US-10-843-527-60965, Sequence 60965, A
c 99 14 3.6 25 22 US-10-843-527-177212, Sequence 177212,
c 100 14 3.6 25 22 US-10-719-956-13264, Sequence 13264, A
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ALIGNMENTS

RESULT 1

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US-10-239-734-20/c
; Sequence 20, Application US/10239734
; Publication No. US20040161746A1
; GENERAL INFORMATION:
; APPLICANT: GENOX RESEARCH, INC.
; APPLICANT: JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR
; APPLICANT: CHILD HEALTH AND DEVELOPMENT
; APPLICANT: Matsumoto, Yoshiko
; APPLICANT: Tsujimoto, Gozoh
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Sugita, Yuji
; APPLICANT: Oshida, Tadairo
; APPLICANT: Imai, Yukiko
; TITLE OF INVENTION: Method of Testing For Allergic Disease
; FILE REFERENCE: SHIMIZU-07379
; CURRENT APPLICATION NUMBER: US/10/239,734
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/JP01/11286
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 2000-389476 JP
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: an artificially synthesized Tagman probe sequence
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(1)
; OTHER INFORMATION: Label FAM (6-carboxy-fluorescein)
; NAME/KEY: misc binding
; LOCATION: (28)..(28)
; OTHER INFORMATION: Label TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine)
US-10-239-734-20
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Query Match 5.2%; Score 20; DB 19; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 218 GAGCTCTATGCGACCAAGA 237
Db 23 GACTCTATGCGACCAAGA 4
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RESULT 2
US-11-036-317-846886/c
; Sequence 846886, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 846886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-846886
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Query Match 4.4%; Score 17; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 111 AGGCCGAGTCTGCGGC 127
Db 25 AGGCCGAGTCTGCGGC 9
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RESULT 3
US-10-719-900-106967/c
; Sequence 106967, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106967
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-106967
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Query Match 4.2%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 50 TTCAATTCCTGGAGCC 65
Db 23 TTCAATTCCTGGAGCC 8
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RESULT 4
US-10-719-900-362302/c
; Sequence 362302, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 ; Search time 117.836 Seconds
(without alignments)
5332.244 Million cell updates/sec

Title: US-09-887-941B-5

Perfect score: 384
Sequence: 1 cagccgcgcgcgcgcgcac.....atgagtgctggcgcgcgt 384

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 81813359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

Issued Patents, NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	16	4.2	25	4	US-09-396-196G-29049
2	15	3.6	50	4	US-09-513-999C-15047
3	14	3.6	20	2	US-09-289-368-69
4	14	3.6	21	3	US-09-311-260-147
5	14	3.6	23	2	US-08-859-998-87
6	14	3.6	23	4	US-09-225-928-87
7	14	3.6	23	4	US-09-225-201B-87
8	14	3.6	25	4	US-09-396-196G-2879
9	14	3.6	25	4	US-09-396-196G-49209
10	14	3.6	25	4	US-09-396-196G-64399
11	14	3.6	25	4	US-09-396-196G-117483
12	14	3.6	42	1	US-08-256-964A-6
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15	13	3.4	18	3	US-09-166-186-167
16	13	3.4	18	3	US-09-166-186-168
17	13	3.4	18	3	US-09-166-186-169
18	13	3.4	18	3	US-09-166-186-170
19	13	3.4	18	3	US-09-313-932-165
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21	13	3.4	18	3	US-09-313-932-167
22	13	3.4	18	3	US-09-313-932-168
23	13	3.4	18	3	US-09-313-932-169
24	13	3.4	18	3	US-09-313-932-170
25	13	3.4	20	2	US-08-907-492A-8
26	13	3.4	20	2	US-08-166-186-146
27	13	3.4	20	3	US-09-166-186-147

28	13	3.4	20	3	US-09-166-186-148	Sequence 148, App
29	13	3.4	20	3	US-09-166-186-149	Sequence 149, App
30	13	3.4	20	3	US-09-166-186-150	Sequence 150, App
31	13	3.4	20	3	US-09-166-186-151	Sequence 151, App
32	13	3.4	20	3	US-09-166-186-152	Sequence 152, App
33	13	3.4	20	3	US-09-166-186-153	Sequence 153, App
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41	13	3.4	20	3	US-09-313-932-153	Sequence 153, App
42	13	3.4	20	3	US-09-489-868A-55	Sequence 153, App
43	13	3.4	20	4	US-09-544-358B-194	Sequence 194, App
44	13	3.4	21	4	US-09-543-771B-194	Sequence 194, App
45	13	3.4	21	4	US-09-422-978-10994	Sequence 10994, A
46	13	3.4	22	1	US-08-287-075-7	Sequence 7, Appl
47	13	3.4	22	3	US-07-974-409C-11	Sequence 11, Appl
48	13	3.4	22	3	US-07-974-409C-312	Sequence 312, App
49	13	3.4	22	4	US-09-269-446D-102	Sequence 102, App
50	13	3.4	22	5	PCT-US93-00977-11	Sequence 11, Appl
51	13	3.4	22	5	PCT-US93-00977-312	Sequence 312, App
52	13	3.4	24	4	US-09-093-972C-970	Sequence 970, App
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54	13	3.4	25	4	US-09-396-196G-21199	Sequence 21199, A
55	13	3.4	25	4	US-09-396-196G-24204	Sequence 24204, A
56	13	3.4	25	4	US-09-396-196G-24902	Sequence 24902, A
57	13	3.4	25	4	US-09-396-196G-24903	Sequence 24903, A
58	13	3.4	25	4	US-09-396-196G-24904	Sequence 24904, A
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60	13	3.4	25	4	US-09-396-196G-28058	Sequence 28058, A
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76	13	3.4	28	3	US-09-356-281-9	Sequence 9, Appl
77	13	3.4	30	3	US-08-685-871-4	Sequence 4, Appl
78	13	3.4	30	3	US-08-685-871-6	Sequence 6, Appl
79	13	3.4	30	3	US-09-270-140A-94	Sequence 94, Appl
80	13	3.4	39	3	US-08-585-684B-85	Sequence 85, Appl
81	12	3.1	15	2	US-08-585-684B-86	Sequence 86, Appl
82	12	3.1	15	2	US-09-038-073-85	Sequence 85, Appl
83	12	3.1	15	3	US-09-038-073-86	Sequence 86, Appl
84	12	3.1	15	3	US-09-081-646-179	Sequence 179, App
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86	12	3.1	16	1	US-08-142-845-2	Sequence 2, Appl
87	12	3.1	16	1	US-08-142-845-3	Sequence 3, Appl
88	12	3.1	16	1	US-08-142-845-4	Sequence 4, Appl
89	12	3.1	16	1	US-08-483-746A-2	Sequence 2, Appl
90	12	3.1	16	3	US-08-483-746A-3	Sequence 3, Appl
91	12	3.1	16	3	US-08-483-746A-4	Sequence 4, Appl
92	12	3.1	16	3	US-08-483-746A-5	Sequence 5, Appl
93	12	3.1	18	1	US-08-058-907-2	Sequence 2, Appl
94	12	3.1	18	1	US-08-487-748A-18	Sequence 18, Appl
95	12	3.1	18	2	US-08-585-684B-293	Sequence 293, Ap
96	12	3.1	18	2	US-08-767-979-25	Sequence 25, Appl
97	12	3.1	18	3	US-08-398-633-9	Sequence 9, Appl
98	12	3.1	18	3	US-08-480-070C-18	Sequence 18, Appl
99	12	3.1	18	3	US-09-166-186-164	Sequence 164, App
100	12	3.1	18	3		

ALIGNMENTS

RESULT 1
US-09-396-196G-29049

Sequence 29049, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for windows Version 4.0

SEQ ID NO 29049

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-09-396-196G-29049

Query Match

Best Local Similarity 100.0%; Score 16; DB 4; Length 25;
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

DB 3 TGTGTCCACAGAGTG 18

RESULT 2
US-09-513-999C-15047/C

Sequence 15047, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59, US2, REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 15047

LENGTH: 50

TYPE: DNA

ORGANISM: Homo sapiens

US-09-513-999C-15047

Query Match

Best Local Similarity 100.0%; Score 15; DB 4; Length 50;
Pred. No. 6.1e+02; Mismatches 0; Indels 0; Gaps 0;

DB 29 TTTCCCTGCCCCACA 15

RESULT 3
US-09-289-368-69/C

Sequence 69, Application US/09289368

Patent No. 5998148

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROTUBULE-ASSOCIATED PROTEIN 4 EXPRESSIC

FILE REFERENCE: RTS-0051

CURRENT APPLICATION NUMBER: US/09/289,368

CURRENT FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 87

SEQ ID NO 69

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-289-368-69

Query Match

Best Local Similarity 100.0%; Score 14; DB 2; Length 20;
Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;DB 90 CCTGCCCCACACC 103
18 CCTGCCCCACACC 5RESULT 4
US-09-311-260-147

Sequence 147, Application US/09311260

Patent No. 6214555

GENERAL INFORMATION:

APPLICANT: Leusner, James

APPLICANT: Hui, May

APPLICANT: Dunn, James M.

APPLICANT: Lacroix, Jean-Michel

TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR DETECTION OF

TITLE OF INVENTION: MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESSES:

ADDRESS: Opedahl & Larson LLP

STREET: P.O. Box 5270

CITY: Prisco

STATE: CO

COUNTRY: US

ZIP: 80443-5270

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/311,260

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Larson, Marina T.

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: VGEN-P-058-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (970) 668-2050

TELEFAX: (970) 668-2082

TELEX:

INFORMATION FOR SEQ ID NO: 147:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: no

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 2670.9 Seconds
(without alignments)
5472.564 Million cell updates/sec

Title: US-09-887-941B-5

Perfect score: 384
Sequence: 1 caggccgcgcgagactccac.....atgagtgctggagccgcgcgc 384

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database:

EST: *
1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	3.6	34	7 W70854	W70854 md91f05..x1
C 2	14	3.6	36	8 A2794093	A2794093 2M0047012
C 3	14	3.6	40	1 A1619480	A1619480 LY38904.x
C 4	14	3.6	47	1 B2381951	B2381951 SALK_1176
C 5	14	3.6	50	1 AUI06633	AUI06633 AUI06633
C 6	13	3.4	28	8 A2308339	A2308339 IM0011A18
C 7	13	3.4	28	9 AG265512	AG265512 locusts cor
C 8	13	3.4	35	5 B0594628	B0594628 EP94a05..8
C 9	13	3.4	37	1 A1928854	A1928854 2P34a05..8
C 10	13	3.4	38	1 AUI257194	AUI257194 AUI257194
C 11	13	3.4	40	1 AA654389	AA654389 mt62d05..8
C 12	13	3.4	40	1 AUI257305	AUI257305 AUI257305
C 13	13	3.4	41	8 R34628	R34628 Y957G12..x1
C 14	13	3.4	41	8 BH796123	BH796123 1008092H0
C 15	13	3.4	41	9 AB081895	AB081895 Drosophila
C 16	13	3.4	42	8 A2770413	A2770413 IM0572B01
C 17	13	3.4	42	8 BX244387	BX244387 Dantio rer
C 18	13	3.4	44	9 BX001979	BX001979 Arabidops
C 19	13	3.4	45	8 A2809363	A2809363 2M0073014
C 20	13	3.4	47	9 AG204311	AG204311 Pan trogl
C 21	13	3.4	48	8 B2357549	B2357549 SALK_1308
C 22	13	3.4	49	9 CU518625	CU518625 DAE7B03..F
C 23	12	3.1	21	1 AUI668099	AUI668099 AUI668099
C 24	12	3.1	21	8 A2991096	A2991096 2M0275C09

C 25	12	3.1	23	9 AG202483	AG202483 Pan trogl1
C 26	12	3.1	25	8 A2782142	A2782142 2M0022H10
C 27	12	3.1	31	1 A1017748	A1017748 cv28d11..x
C 28	12	3.1	31	8 B2380518	B2380518 SALK_1152
C 29	12	3.1	34	5 BQ789855	BQ789855 hage003ac
C 30	12	3.1	34	9 AL758714	AL758714 Arabidops
C 31	12	3.1	35	4 B1251471	B1251471 602994012
C 32	12	3.1	37	1 AA059414	AA059414 2195a02..r
C 33	12	3.1	37	8 B615126	B615126 KG04302..3
C 34	12	3.1	38	4 B1650875	B1650875 603297785
C 35	12	3.1	38	4 B1687189	B1687189 603307847
C 36	12	3.1	38	4 A2657875	A2657875 1M0534A19
C 37	12	3.1	39	9 AG203147	AG203147 Pan trogl1
C 38	12	3.1	40	4 B1693481	B1693481 603343864
C 39	12	3.1	40	7 W72170	W72170 z661d05..81
C 40	12	3.1	40	8 AJS94690	AJS94690 Arabidops
C 41	12	3.1	41	8 B2291498	B2291498 SALK_1208
C 42	12	3.1	41	9 TAL192A12Q	TAL192A12Q T. brucei
C 43	12	3.1	42	1 B1558371	B1558371 603197760
C 44	12	3.1	42	4 B1553162	B1553162 AG0457..Sa
C 45	12	3.1	42	9 CL459321	CL459321 601505866
C 46	12	3.1	44	2 BE882963	BE882963 601505866
C 47	12	3.1	45	1 AAI04422	AAI04422 mo42d06..r
C 48	12	3.1	45	4 BF981238	BF981238 602309544
C 49	12	3.1	45	4 BG700027	BG700027 602681027
C 50	12	3.1	45	8 A2862434	A2862434 2M0170B10
C 51	12	3.1	46	1 AA649959	AA649959 n555d03..s
C 52	12	3.1	46	4 B1647149	B1647149 603279958
C 53	12	3.1	46	4 B910800	B910800 SALK_0626
C 54	12	3.1	47	8 A2815318	A2815318 2M0083A03
C 55	12	3.1	47	8 B2660923	B2660923 SALK_0243
C 56	12	3.1	48	1 AA778526	AA778526 af85h03..s
C 57	12	3.1	48	8 A2795941	A2795941 2M0051L20
C 58	12	3.1	48	9 AL765660	AL765660 Arabidops
C 59	12	3.1	49	1 AA727650	AA727650 v187e07..r
C 60	12	3.1	49	4 BU000359	BU000359 BU000359
C 61	12	3.1	50	1 AUI03795	AUI03795 AUI03795
C 62	12	3.1	50	1 AUI04889	AUI04889 AUI04889
C 63	12	3.1	50	1 AUI05869	AUI05869 AUI05869
C 64	12	3.1	50	1 AUI07916	AUI07916 AUI07916
C 65	12	3.1	50	4 B1651733	B1651733 603298518
C 66	12	2.9	17	8 A2633696	A2633696 1M0489001
C 67	11	2.9	20	8 A2308068	A2308068 1M0010N08
C 68	11	2.9	20	8 A2308311	A2308311 1M001J112
C 69	11	2.9	21	8 A2511925	A2511925 1M0357L09
C 70	11	2.9	21	8 A2626965	A2626965 1M0467B15
C 71	11	2.9	22	8 A2793094	A2793094 2M0045H20
C 72	11	2.9	23	8 A2779607	A2779607 2M0016E18
C 73	11	2.9	23	9 TAL15F09Q	TAL15F09Q T. brucei
C 74	11	2.9	24	8 A2844396	A2844396 2M0143B22
C 75	11	2.9	24	9 CL670227	CL670227 PRI0161C
C 76	11	2.9	25	8 A2303786	A2303786 1M0003G05
C 77	11	2.9	25	8 A2394252	A2394252 1M0157B16
C 78	11	2.9	25	8 A2776639	A2776639 2M0010L02
C 79	11	2.9	25	9 AG189879	AG189879 Pan trogl1
C 80	11	2.9	27	8 A2404479	A2404479 1M0172F18
C 81	11	2.9	28	1 A2779701	A2779701 2M0016M22
C 82	11	2.9	28	1 AA960907	AA960907 0M92C04..s
C 83	11	2.9	28	8 A2466703	A2466703 1M0277N06
C 84	11	2.9	28	8 A2605911	A2605911 1M0427H01
C 85	11	2.9	28	8 A2632301	A2632301 1M0486C23
C 86	11	2.9	29	1 AL045592	AL045592 DKFZP343N
C 87	11	2.9	29	8 A2331636	A2331636 1M0059O09
C 88	11	2.9	29	8 A2335953	A2335953 1M0066E05
C 89	11	2.9	29	8 A2822977	A2822977 2M0096C09
C 90	11	2.9	29	8 A2847949	A2847949 2M0148B23
C 91	11	2.9	29	8 BH864803	BH864803 SALK_0968
C 92	11	2.9	29	8 CC457201	CC457201 SALK_1072
C 93	11	2.9	30	1 AL045336	AL045336 DKFZP434A
C 94	11	2.9	30	1 AL045352	AL045352 DKFZP434B
C 95	11	2.9	30	1 AL045477	AL045477 DKFZP434H
C 96	11	2.9	30	1 AL045487	AL045487 DKFZP434I
C 97	11	2.9	30	4 BM398771	BM398771 5009-0-5-

98 11 2.9 30 7 CK151329
99 11 2.9 30 8 AZ211581
c 100 11 2.9 31 1 AA779867

CK151329 GS1-128 S
AZ211581 IM0027005
AA779867 at4eall.s

ALIGNMENTS

RESULT 1
LOCUS W70854/c
DEFINITION W70854 34 bp mRNA linear EST 17-JUN-1996
md91f05.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA
clone IMAGE:385377 5' similar to SW:HCDD.PIG P00348
3-HYDROXYACYL-CoA DEHYDROGENASE ; mRNA sequence.

ACCESSION W70854
VERSION W70854.1 GI:1381006
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, D., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watsen.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:237209

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: mob.REGA+ET
High quality sequence stop: 1.

FEATURES
Source location/Qualifiers

1..34
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:385377"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NDME13.5 14.5"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCCGCGAATTTTCTTTTCTTTTCTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2 1/2 double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRTT3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."

ORIGIN

Query Match 3.6%; Score 14; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 TATGCACCAAGAG 238
Db 18 TATGCACCAAGAG 5

RESULT 2
LOCUS AZ794093/c
DEFINITION AZ794093 36 bp DNA linear GSS 16-FEB-2001
2M0047012R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
clone UNGC2M0047012 R, genomic survey sequence.

ACCESSION AZ794093
VERSION AZ794093.1 GI:12939709
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D. Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Spd Error: 0.00
Plate: 0047 row: 0 column: 12

Seq primer: CACACAGGAACGCTATGACC
Class: Plasmid ends
High quality sequence stop: 36.

FEATURES
Source location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG2M0047012"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGC1M library"
/note="Vector: FMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G14732114|gb|AF12972.11), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 3.6%; Score 14; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 / Search time 403.806 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-5
Perfect score: 384
Sequence: 1 caggccgcgcgcgcgcgcac.....atgagctgtggcaccgcgcgt 384

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

1: N_Geneseq_16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	5.7	22	AD030502	AD030502 Human nov
2	20	5.2	28	AA149965	AA149965 B1153 exp
3	15	3.9	19	ABD31263	ABD31263 Human CD2
4	15	3.9	19	ADJ60097	ADJ60097 Oligonuc1
5	15	3.9	19	AD045566	AD045566 Human o11
6	15	3.9	22	AAV51970	AAV51970 Zea may8
7	15	3.9	25	ACKI1732	ACKI1732 Human mic
8	15	3.9	25	ACK02627	ACK02627 Human mic
9	15	3.9	25	ACI56494	ACI56494 Human mic
10	15	3.9	25	ACI13536	ACI13536 Human mic
11	15	3.9	25	ACI92185	ACI92185 Human mic
12	15	3.9	25	ACI14985	ACI14985 Human mic
13	15	3.9	29	AAV70828	AAV70828 Molecular
14	15	3.9	40	AAV51134	AAV51134 Maize pol
15	15	3.9	42	AAV71123	AAV71123 Molecular
16	15	3.9	42	AAV71114	AAV71114 Molecular
17	15	3.9	42	AAV71119	AAV71119 Molecular
18	15	3.9	42	AAV71131	AAV71131 Molecular
19	15	3.9	42	AAV71127	AAV71127 Molecular
20	15	3.9	45	AAV70824	AAV70824 Molecular

C	21	15	3.9	46	3	AAV71094	AAV71094 Molecular
C	22	15	3.9	46	3	AAV71110	AAV71110 Molecular
C	23	15	3.9	46	3	AAV71087	AAV71087 Molecular
C	24	15	3.9	46	3	AAV71096	AAV71096 Molecular
C	25	15	3.9	46	3	AAV71099	AAV71099 Molecular
C	26	15	3.9	46	3	AAV71100	AAV71100 Molecular
C	27	15	3.9	46	3	AAV71104	AAV71104 Molecular
C	28	15	3.9	50	3	AAV71092	AAV71092 Human sec
C	29	14	3.6	17	3	AAV71092	AAV71092 Human sec
C	30	14	3.6	17	12	ADP183762	ADP183762 HCV DNAzy
C	31	14	3.6	20	3	AAV70854	AAV70854 Human mic
C	32	14	3.6	20	12	ADP183762	ADP183762 HCV DNAzy
C	33	14	3.6	20	12	ADP183762	ADP183762 HCV DNAzy
C	34	14	3.6	20	12	ADP183762	ADP183762 HCV DNAzy
C	35	14	3.6	21	4	AAV71123	AAV71123 Molecular
C	36	14	3.6	21	9	AAV71123	AAV71123 Molecular
C	37	14	3.6	23	6	ABK88357	ABK88357 Human nov
C	38	14	3.6	23	6	ABK88357	ABK88357 Human nov
C	39	14	3.6	25	9	ACI22066	ACI22066 Human mic
C	40	14	3.6	28	4	AAV71480	AAV71480 Maguk p55
C	41	14	3.6	28	4	AAV71480	AAV71480 Maguk p55
C	42	14	3.6	28	4	AAV71480	AAV71480 Maguk p55
C	43	14	3.6	28	6	ABT06621	ABT06621 PDZ domai
C	44	14	3.6	28	6	ABT06621	ABT06621 PDZ domai
C	45	14	3.6	28	6	ABT06621	ABT06621 PDZ domai
C	46	14	3.6	29	6	ABT06621	ABT06621 PDZ domai
C	47	14	3.6	29	6	ABT06621	ABT06621 PDZ domai
C	48	14	3.6	31	2	AAV717842	AAV717842 PCR prime
C	49	14	3.6	31	2	AAV717842	AAV717842 PCR prime
C	50	14	3.6	33	10	ADP62529	ADP62529 Human TIR
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C	52	14	3.6	41	6	ABT45546	ABT45546 Novel hum
C	53	14	3.6	41	6	ABT45546	ABT45546 Novel hum
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C	67	14	3.6	50	4	AAV717882	AAV717882 Maize pol
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C	82	14	3.6	50	4	AAV717882	AAV717882 Maize pol
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C	89	14	3.6	50	4	AAV717882	AAV717882 Maize pol
C	90	14	3.6	50	4	AAV717882	AAV717882 Maize pol
C	91	14	3.6	50	4	AAV717882	AAV717882 Maize pol
C	92	14	3.6	50	4	AAV717882	AAV717882 Maize pol
C	93	14	3.6	50	4	AAV717882	AAV717882 Maize pol

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 2356.15 Seconds
(without alignments)
7897.122 Million cell updates/sec

Title: US-09-887-941B-5
Perfect score: 384
Sequence: 1 caggccgcgcgcgactccac.....atgagctgtgggaccgcgcgt 384

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_ov:*
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6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

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LOCUS BD171194/c 28 bp DNA linear PAT 17-JUN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171194
VERSION BD171194.1 GI:27877006
KEYWORDS WO 0250269-A/19.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 19 27-JUN-2002;
GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MAGAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 0250269-A/19
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU,
GOZO TSUJIMOTO
PI GOZO TSUJIMOTO
PC C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
PC A61P37/08,
PC C12Q1/68,G01N33/50
CC Description of Artificial Sequence:an artificially synthesized

COMMENT

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ORIGIN

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DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274271
VERSION BD274271.1 GI:33084039
KEYWORDS JP 2002526030-A/238.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffee,R. and McNeil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery
JOURNAL Patent: JP 2002526030-A 238 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL
PC C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description of Artificial Sequence: Novel Sequence FH Key
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FEATURES

source

ORIGIN

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DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION BD274275
VERSION BD274275.1 GI:33084043
KEYWORDS JP 2002526030-A/242.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffee,R. and McNeil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery
JOURNAL Patent: JP 2002526030-A 242 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/242
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL
PC C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description of Artificial Sequence: Novel Sequence FH Key
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FEATURES

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ORIGIN

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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93 14 9.5 46 22 US-10-973-783-78 Sequence 78, Appl
94 14 9.5 50 9 US-09-727-889-8 Sequence 8, Appl
95 14 9.5 50 20 US-10-849-462-8 Sequence 8, Appl
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97 13 8.8 13 20 US-10-257-017B-33726 Sequence 33726, A
98 13 8.8 17 9 US-09-864-785-640 Sequence 640, App
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ALIGNMENTS

RESULT 1
US-10-751-736-7378

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/ Publication No. US20040265230A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Martinez, Robert
/ APPLICANT: Brown, Eugene
/ APPLICANT: Liu, Wei
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
/ FILE REFERENCE: AM100927 (031896-002000)
/ CURRENT APPLICATION NUMBER: US/10/751,736
/ CURRENT FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
/ PRIOR FILING DATE: 2003-01-06
/ NUMBER OF SEQ ID NOS: 54873
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 7378
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-10-751-736-7378
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Best Local Similarity 100.0%; Pred. No. 56;
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/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Martinez, Robert
/ APPLICANT: Brown, Eugene
/ APPLICANT: Liu, Wei
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
/ FILE REFERENCE: AM100927 (031896-002000)
/ CURRENT APPLICATION NUMBER: US/10/751,736
/ CURRENT FILING DATE: 2003-01-06
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/ PRIOR FILING DATE: 2003-01-06
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US-10-751-736-7379
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US-10-719-900-54731/C
/ Sequence 54731, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 54731
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-54731
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Query Match 11.5% Score 17; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 28 CCCTGCAGCAGCAAG 44
DB 21 CCCTGCAGCAGCAAG 5
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RESULT 4
US-10-751-736-6811

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/ Sequence 6811, Application US/10751736
/ Publication No. US20040265230A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Martinez, Robert
/ APPLICANT: Brown, Eugene
/ APPLICANT: Liu, Wei
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
/ FILE REFERENCE: AM100927 (031896-002000)
/ CURRENT APPLICATION NUMBER: US/10/751,736
/ CURRENT FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
/ PRIOR FILING DATE: 2003-01-06
/ NUMBER OF SEQ ID NOS: 54873
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6811
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-10-751-736-6811
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Query Match 10.8% Score 16; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
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ALIGNMENTS

RESULT 1

US-09-360-416-119
; Sequence 119, Application US/09360416
; Patent No. 6458536
; GENERAL INFORMATION:
; APPLICANT: Richard A. Gatti
; TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
; FILE REFERENCE: 510015-222
; CURRENT APPLICATION NUMBER: US/09360,416
; CURRENT FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-360-416-119

Query Match 10.1%; Score 15; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 TATTTCATTCTTA 65
|||||
Db 5 TATTTCATTCTTA 19

RESULT 2

US-08-160-670A-41
; Sequence 41, Application US/08160670A
; Patent No. 5449758
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Protein Size Marker Ladder
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,670A
FILING DATE: 12/2/93

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmont, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942,2580000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both

US-08-160-670A-41

Query Match 10.1%; Score 15; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 TTTGAGTTGCCACC 80
|||||
Db 4 TTTGAGTTGCCACC 18

RESULT 3

US-09-443-501A-8
; Sequence 8, Application US/09443501A
; Patent No. 6303342
; GENERAL INFORMATION:
; APPLICANT: Kusan Biosciences, Inc.
; APPLICANT: Julien, Bryan
; APPLICANT: Katz, Leonard
; APPLICANT: Khosla, Chaitan
; APPLICANT: Tang, Li
; APPLICANT: Ziermann, Rainer
; TITLE OF INVENTION: Recombinant Methods and Materials for Producing
; FILE REFERENCE: 30062-20031.00
; CURRENT APPLICATION NUMBER: US/09/443,501A
; CURRENT FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 60/130,560
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/122,620
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: US 60/119,386
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/109,401
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-443-501A-8

Query Match 9.5%; Score 14; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 GACCGACCGAGAG 134
|||||
Db 24 GACCGACCGAGAG 37

RESULT 4

US-09-357-072-78/C
; Sequence 78, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-78

98 11 7.4 38 8 AZ382826 AZ382826 1M0140F13
 99 11 7.4 38 8 AZ592469 AZ592469 1M0403K19
 100 11 7.4 38 8 BZ380345 BZ380345 SMLK_1149

ALIGNMENTS

RESULT 1
 A1444400 40 bp mRNA linear EST 07-JUN-2001
 LOCUS FB38a05.x1 Zebrafish Washu MPING EST Danio rerio cDNA clone
 DEFINITION IMAGE:3714128.3 similar to SW:RS8_HUMAN P09058 40S RIBOSOMAL
 PROTEIN S8. /, mRNA sequence.
 ACCESSION A1444400
 VERSION A1444400.1 GI:4281397
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 40)
 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
 Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
 Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck,R.,
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,W., McCann,R.,
 Waterston,R. and Wilson,R.
 Washu Zebrafish EST Project 1998
 Unpublished (1998)
 CONTACT: Stephen L. Johnson
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrfish@wustl.wustl.edu
 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 ResourcenzentrumPrimateBank, Berlin, Germany (web address:
 www.rzpd.de)

Trace considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 Seq primer: T7 ET from Amersham
 High quality sequence stop: 1
 POLYA=NO.

FEATURES

source
 1..40
 /location/Qualifiers
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:3714128"
 /sex="mixed"
 /tissue-type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="XLI-blue MRF"
 /clone_lib="Zebrafish Washu MPING EST"
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
 strand cDNA was primed with a Not I - oligo(dn)15 primer
 (5'-GACACTGCTCAGATCGGAGCGCCGCTTTTCTTTTCTTTT3');
 double-stranded cDNA was ligated to Sal I adaptor (BRL),
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehrach lab), ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 som) adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint

ORIGIN

Query Match 9.5%; Score 14; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 74 TGGCACCACCAACAA 87
 2 TGGCACCACCAACAA 15

RESULT 2
 A2591573 44 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0401E18R Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone UGCLM0401E15 R, genomic survey sequence.
 ACCESSION A2591573
 VERSION A2591573.1 GI:11713763
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 44)
 Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0401 row: B column: 15
 Seq primer: CACACAGAAACAGCTATGAC
 Class: Plasmid ends
 High quality sequence stop: 44.

TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1..44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0401E15"
 /sex="Male"
 /lab_host="E. Coli strain XLI-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 155.633 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941b-4

Perfect score: 148
Sequence: 1 ttgcgcgcagtcacgaac.....gagaagaagagcctcccg 148

Scoring table: OLIGO_NTIC
Gapop 60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

1: N_Geneseq_16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2002bs:*
9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	10.1	19	2	AAZ10229
C 2	15	10.1	20	4	AAF60217
C 3	15	10.1	30	2	AAT04991
C 4	14	9.5	20	10	ABD34057
C 5	14	9.5	20	11	ABD30287
C 6	14	9.5	21	3	AAC64373
C 7	14	9.5	23	6	AAD52722
C 8	14	9.5	25	6	AAD27200
C 9	14	9.5	25	9	ACI16144
C 10	14	9.5	25	9	ACI14845
C 11	14	9.5	28	13	ADR32546
C 12	14	9.5	32	13	ADR33205
C 13	14	9.5	43	6	ABZ26875
C 14	14	9.5	50	3	AAA29355
C 15	13	8.8	13	5	ABC33708
C 16	13	8.8	13	5	ABC33709
C 17	13	8.8	17	3	AAF07081
C 18	13	8.8	17	8	ACA06862
C 19	13	8.8	17	8	ACA07862
C 20	13	8.8	17	8	ACA06821

C 21	13	8.8	17	8	ACC63011	ACC63011 Murine ol
C 22	13	8.8	19	12	ADF91918	ADF91918 Human cyC
C 23	13	8.8	19	12	ADF92115	ADF92115 Human cyC
C 24	13	8.8	19	12	ADG62153	ADG62153 Anti-FADD
C 25	13	8.8	19	13	ADR76043	ADR76043 Human apo
C 26	13	8.8	19	13	ADR78661	ADR78661 Human apo
C 27	13	8.8	20	2	AAT99894	AAT99894 Primer OM
C 28	13	8.8	20	2	AAT99895	AAT99895 Primer OM
C 29	13	8.8	20	2	AAT99896	AAT99896 Primer OM
C 30	13	8.8	20	2	AAT98090	AAT98090 Chlamydia
C 31	13	8.8	20	2	AAT98089	AAT98089 Chlamydia
C 32	13	8.8	20	3	AAZ44822	AAZ44822 Human FAD
C 33	13	8.8	20	3	AAA47901	AAA47901 Chlamydia
C 34	13	8.8	20	3	AAA65807	AAA65807 Chlamydia
C 35	13	8.8	20	3	AAA65808	AAA65808 Chlamydia
C 36	13	8.8	20	4	AAB02989	AAB02989 C trachom
C 37	13	8.8	20	4	AAH02990	AAH02990 C trachom
C 38	13	8.8	20	4	AAH02991	AAH02991 C trachom
C 39	13	8.8	20	4	ABT15797	ABT15797 Human GU
C 40	13	8.8	20	9	ACF05746	ACF05746 Bcl2 sens
C 41	13	8.8	20	9	ADA27414	ADA27414 Micoorgan
C 42	13	8.8	20	9	ADA27415	ADA27415 Micoorgan
C 43	13	8.8	20	9	ADA27413	ADA27413 Micoorgan
C 44	13	8.8	20	10	ABZ94058	ABZ94058 Human ol
C 45	13	8.8	20	11	ABD30288	ABD30288 HOS914-de
C 46	13	8.8	20	12	ADF91920	ADF91920 Human cyC
C 47	13	8.8	20	12	ADF91919	ADF91919 Human cyC
C 48	13	8.8	20	12	ADF92116	ADF92116 Human cyC
C 49	13	8.8	20	12	ADG86687	ADG86687 Human APP
C 50	13	8.8	21	12	AD016005	AD016005 4 synthes
C 51	13	8.8	22	12	ADK41285	ADK41285 Human chr
C 52	13	8.8	22	12	ADK41395	ADK41395 Human chr
C 53	13	8.8	22	12	ADK41395	ADK41395 Human chr
C 54	13	8.8	23	6	ABT08556	ABT08556 Human nov
C 55	13	8.8	23	8	AA54151	AA54151 NOVX rela
C 56	13	8.8	23	12	AD009921	AD009921 Human NOV
C 57	13	8.8	23	12	AD041932	AD041932 Novel hum
C 58	13	8.8	24	6	ABK69681	ABK69681 Human WTI
C 59	13	8.8	24	6	ABZ30370	ABZ30370 Candida a
C 60	13	8.8	24	6	ABE61809	ABE61809 Analyt s
C 61	13	8.8	24	6	AB187774	AB187774 Capture o
C 62	13	8.8	24	6	AB187775	AB187775 Capture o
C 63	13	8.8	24	10	ADB67557	ADB67557 Human WTI
C 64	13	8.8	24	10	ADB080790	ADB080790 Wilms' tu
C 65	13	8.8	24	12	ADU83710	ADU83710 PCR prime
C 66	13	8.8	24	12	ADU57598	ADU57598 Human tru
C 67	13	8.8	25	12	AD009153	AD009153 Truncated
C 68	13	8.8	25	9	ACD06297	ACD06297 RT-PCR pr
C 69	13	8.8	25	9	ACI65526	ACI65526 Human mic
C 70	13	8.8	25	9	ACI11414	ACI11414 Human mic
C 71	13	8.8	25	9	ACI12050	ACI12050 Human mic
C 72	13	8.8	25	9	ACK08719	ACK08719 Human mic
C 73	13	8.8	25	9	ACI24980	ACI24980 Human mic
C 74	13	8.8	25	9	ACI15507	ACI15507 Human mic
C 75	13	8.8	25	9	ACI10776	ACI10776 Human mic
C 76	13	8.8	25	9	ACI10140	ACI10140 Human mic
C 77	13	8.8	25	9	ACI194368	ACI194368 Human mic
C 78	13	8.8	25	9	ACH51016	ACH51016 DNA targe
C 79	13	8.8	25	9	ACH52593	ACH52593 DNA targe
C 80	13	8.8	25	9	ACH51015	ACH51015 DNA targe
C 81	13	8.8	25	12	ADN96735	ADN96735 Human NOV
C 82	13	8.8	25	12	ADN16726	ADN16726 Renal cel
C 83	13	8.8	25	12	ADP16724	ADP16724 Renal cel
C 84	13	8.8	25	12	ADP16725	ADP16725 Renal cel
C 85	13	8.8	26	6	ABK66694	ABK66694 Human gen
C 86	13	8.8	27	10	ADK17672	ADK17672 HeLa cell
C 87	13	8.8	30	6	ABX75581	ABX75581 Novel Hei
C 88	13	8.8	32	6	ABK16403	ABK16403 Human adi
C 89	13	8.8	32	12	ADP66736	ADP66736 Human adi
C 90	13	8.8	33	3	AAA15731	AAA15731 PCR prime
C 91	13	8.8	33	6	ABK48783	ABK48783 PCR prime
C 92	13	8.8	35	3	ABK50828	ABK50828 Cyclin de
C 93	13	8.8				

	94	13	8.8	35	4	AAf24618
C	95	13	8.8	36	2	AAV46359
C	96	13	8.8	37	12	Adf92158
C	97	13	8.8	37	12	Adf92158
C	98	13	8.8	39	4	AAf24615
C	99	13	8.8	41	6	ABZ46601
C	100	13	8.8	41	6	ABZ44247

ALIGNMENTS

	Query Match	10.1%;	Score 15;	DB 2;	Length 19;
	Best Local Similarity	100.0%;	Pred. No. 1.1e+03;		
	Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

33 GCAGCAGCAAGCCA 47
 |||||
 15 GCAGCAGCAAGCCA 1

RESULT 2
 AAF60217
 ID AAF60217 standard; DNA, 20 BP.

AC AAF60217;
 DT 27-APR-2001 (first entry)
 DE Human ATM gene exon 53 reverse primer.

KW Human; ATM; ataxia telangiectasia; mutation detection;
 KW single-stranded conformation polymorphism; SSCP; electrophoresis;
 KW PCR primer; ss.

OS Homo sapiens.

PN MO200107660-A1.

PD 01-FEB-2001.

PF 21-JUL-2000; 2000WO-US020011.

PR 23-JUL-1999; 99US-00360416.

PA (REGC) UNIV CALIFORNIA.

PI Gatti RA;

DR MPI; 2001-168574/17.

PT Detecting a mutation or polymorphism in human ataxia telangiectasia gene
 PT or polyexonic eukaryotic gene, involves using mega-single stranded
 PT conformation polymorphism analysis.

PS Claim 7; Page 54; 118pp; English.

XX The present sequence is one of a number of primers used in a method for
 CC detecting a mutation or a polymorphism in the human ATM gene, which is
 CC associated with the disease ataxia telangiectasia, or a polyexonic
 CC eukaryotic gene of at least 4 kb. The method uses an improved version of
 CC single-stranded conformation polymorphism (SSCP) electrophoresis that
 CC allows electrophoresis of two or three amplified segments in a single
 CC lane. The method is useful for screening large, complex polyexonic
 CC eukaryotic genes such as the ATM gene for mutations and polymorphisms.
 CC The new mutations and polymorphisms in the ATM gene are useful for
 CC performing more accurate screening of human DNA samples for mutations,
 CC for distinguishing mutations from polymorphisms, and for improving the
 CC efficiency of automated screening methods. The mega-SSCP method provides
 CC a screening method of genes for multiple polymorphisms and mutations at
 CC once. The method is particularly suitable for large, polyexonic,
 CC eukaryotic genes, having mutations and polymorphisms at many points and
 CC not merely at one or a few hot spots. Note: the SEQ ID assigned to this
 CC sequence in the disclosure and claims of the specification is one
 CC number lower than the number given in the sequence listing

XX Sequence 20 BP; 3 A; 3 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 10.1%; Score 15; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 TATTCGATTTCTTA 65
 |||||

RESULT 1
 AA210229/c
 ID AA210229 standard; DNA, 19 BP.
 AC AA210229;
 DT 01-NOV-1999 (first entry)
 DE Oligonucleotide probe P6 used to detect a Met receptor.
 XX Hepatocyte growth factor; HGF; axonal growth; sympathetic neuron;
 KW axonal regeneration; axonal degeneration; post-natal neuron; neuropathy;
 KW motor neuropathy; diabetic neuropathy; distal sensory; sensorimotor;
 KW autonomic; visceral autonomic polynuropathy; mononeuropathy;
 KW mononeuropathy multiplex; foot ulceration; cardiac arrhythmia;
 KW sexual impotence; chronic pain; abnormal vascular response; infection;
 KW ischemia; toxin exposure; radiation; Met receptor; probe; ss.
 XX Synthetic.
 OS Mus sp.
 PN WO936103-A1.
 PD 22-JUL-1999.
 PF 15-JAN-1999; 99MO-US000965.
 PR 16-JAN-1998; 98US-00071694.
 PA (UYMC-) UNIV MCGILL.
 PI Miller FD, Yang X;
 DR MPI; 1999-527196/44.
 PT Novel methods for preventing axonal degeneration and promoting axonal
 PT growth using hepatocyte growth factor.
 XX Example 1; Page 21; 65pp; English.
 XX The present sequence represents a probe used to detect a Met receptor.
 CC The Met receptor is the cognate receptor for hepatocyte growth factor
 CC (HGF), which is used to promote axonal growth. Localized exogenous HGF
 CC promotes the growth (but not the survival) of sympathetic neurons. HGF
 CC specification describes a method for promoting axonal growth or axonal
 CC regeneration, or for inhibiting axonal degeneration, of a post-natal
 CC neuron. The method comprises administering an expression vector,
 CC comprising HGF gene operably linked to a promoter, to the neuron. HGF may
 CC be used for treating or inhibiting neuropathy in a patient. The
 CC neuropathy may be symptomatic or asymptomatic, caused by axonal
 CC degeneration, and is an autonomic, sensory, a sensorimotor or a motor
 CC neuropathy and a diabetic neuropathy (especially distal sensory,
 CC sensorimotor, autonomic and visceral autonomic polynuropathy, and
 CC mononeuropathy, or mononeuropathy multiplex). HGF may also be used in the
 CC treatment of foot ulceration, cardiac arrhythmia, sexual impotence,
 CC chronic pain or abnormal vascular responses. HGF may be used to promote
 CC axonal growth and regeneration, for the prevention or treatment of
 CC neuropathies involving axonal degeneration, e.g. infection, ischemia,
 CC toxin exposure, radiation
 XX Sequence 19 BP; 1 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 908.099 Seconds
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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	14	9.5	50	6 AR172670	AR172670 Sequence
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9	13	8.8	17	6 BD259279	BD259279 Regulatio
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14	13	8.8	20	6 AR266147	AR266147 Sequence
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C 37	13	8.8	41	6	AR431932	AR431932 Sequence
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ALIGNMENTS

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 LOCUS BOVINE43
 DEFINITION Bovine DNA for microsatellite marker, 3' terminus.
 ACCESSION D83323
 VERSION D83323.1 GI:1199740
 KEYWORDS PCR primer.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (sites)
 Hirono, T., Nakane, S., Mizoshita, K., Yamakuchi, H.,
 Inoue-Murayama, M., Watanabe, T., Barendse, W. and Sugimoto, Y.
 Characterization of 42 highly polymorphic bovine microsatellite
 markers
 JOURNAL Anim. Genet. 27 (5), 365-368 (1996)
 MEDLINE 97083737
 PUBMED 8930081
 2 (bases 1 to 20)
 Hirono, T., Nakane, S., Mizoshita, K., Inoue-Murayama, M., Watanabe, T.,
 Barendse, W. and Sugimoto, Y.
 Characterization of 42 bovine microsatellite markers
 TITLE Unpublished
 JOURNAL 3 (bases 1 to 20)
 AUTHORS Sugimoto, Y.
 DIRECT SUBMISSION
 SUBMITTED (29-JAN-1996) Yoshikazu Sugimoto, Japan Live Stock
 Technology Association, Shitakawa Institute of Animal Genetics;
 Nishio Oshikawa, Nishiohikawa, Fukushima 961, Japan
 (E-mail: LD103222@niftyserve.or.jp, Tel:0246-25-5641,
 Fax:0248-25-5725)
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 1 GCCTGAGGCGAGGAA 15
 RESULT 2 20 bp DNA linear PAT 20-DEC-2002
 LOCUS AR233757
 DEFINITION Sequence 119 from patent US 6458536.
 ACCESSION AR233757
 VERSION AR233757.1 GI:27276381
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

Unclassified.
 1 (bases 1 to 20)

REFERENCE 1 (bases 1 to 20)
 AUTHORS Gatti, R.A.
 TITLE Modified SSCP method using sequential electrophoresis of multiple
 nucleic acid segments

JOURNAL Patent: US 6458536-A 119 01-OCT-2002;
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 5 TATTCGATTCCTTA 19

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LOCUS 114415 30 bp DNA linear PAT 26-SEP-1995
 DEFINITION Sequence 41 from patent US 5449758.
 ACCESSION 114415
 VERSION 114415.1 GI:996901
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Hartley, J.L.
 TITLE Protein size marker ladder
 JOURNAL Patent: US 5449758-A 41 12-SEP-1995;
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 4 TTTCAGTTGCCACC 18

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 LOCUS BD275574
 DEFINITION Novel Human Voltage-Gated Potassium Channel.
 ACCESSION BD275574
 VERSION BD275574.1 GI:33085342
 KEYWORDS JP 2002543768-A/4.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
 Metzker, M.L., Li, W., Petrukhin, K. and Caskey, T.C.
 Novel Human Voltage-Gated Potassium Channel
 Patent: JP 2002543768-A 4 24-DEC-2002;

JOURNAL Merck and Co Inc

COMMENT OS Homo Sapiens

PN JP 2002543768-A/4

PD 24-DEC-2002

PF 10-APR-2000 JP 200611548

PR 14-APR-1999 US 60/129274

PI Michael I metzker, wen li, konstantin petrukhin, thomas c caskey

CC

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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85 14 7.9 25 24 US-11-036-317-906120 Sequence 906120.
86 14 7.9 26 17 US-10-381-779-75 Sequence 75, Appl
87 14 7.9 33 15 US-10-079-709-35 Sequence 35, Appl
88 13 7.3 17 10 US-09-818-875-3070 Sequence 3070, Ap
89 13 7.3 17 10 US-09-818-875-3071 Sequence 3071, Ap
90 13 7.3 17 17 US-10-209-787-3070 Sequence 3070, Ap
91 13 7.3 17 17 US-10-209-787-3071 Sequence 3071, Ap
92 13 7.3 17 17 US-10-261-185-3070 Sequence 3070, Ap
93 13 7.3 17 17 US-10-261-185-3071 Sequence 3071, Ap
94 13 7.3 17 19 US-10-681-074-3070 Sequence 3070, Ap
95 13 7.3 17 19 US-10-681-074-3071 Sequence 3071, Ap
96 13 7.3 18 17 US-10-349-607-96 Sequence 96, Appl
97 13 7.3 19 17 US-10-444-925-88 Sequence 88, Appl
98 13 7.3 19 17 US-10-444-925-89 Sequence 89, Appl
99 13 7.3 19 17 US-10-444-925-153 Sequence 153, Appl
100 13 7.3 19 17 US-10-444-925-226 Sequence 226, Appl
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ALIGNMENTS

RESULT 1
US-11-036-317-435950/C
Sequence 435950, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 435950

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-435950

Query Match 9.6%; Score 17; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 CTCCTGTTCCGAGCTA 49
Db 25 CTCCTGTTCCGAGCTA 9

RESULT 2
US-11-036-317-939697

Sequence 939697, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 939697

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus
US-11-036-317-939697

Query Match 9.6%; Score 17; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 CCTTCCAGGGCCAGCC 139
Db 2 CCTTCCAGGGCCAGCC 18

RESULT 3
US-11-036-317-980948

Sequence 980948, Application US/11036317
Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 980948

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-980948

Query Match 9.6%; Score 17; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 CCTTCCAGGGCCAGCC 139
Db 4 CCTTCCAGGGCCAGCC 20

RESULT 4
US-10-085-188-4/C

Sequence 4, Application US/10085188
Publication No. US20030032778A1

GENERAL INFORMATION:
APPLICANT: Preenell, Scott R.

APPLICANT: Taft, David W.

TITLE OF INVENTION: A New Member of the Human

FILE REFERENCE: 98-69

CURRENT APPLICATION NUMBER: US/10/085,188

CURRENT FILING DATE: 2002-02-26

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: PCR primer

US-10-085-188-4

Query Match 8.5%; Score 15; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TTCCACGACGCG 64
Db 18 TTCCACGACGCG 4

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OM nucleic - nucleic search, using ew model

Run on: October 7, 2005, 23:25:05 ; Search time 54.315 Seconds
(without alignments)
5332.244 Million cell updates/sec

Title: US-09-887-941B-3

Perfect score: 177

Sequence: 1 gcttcctttctcgctt.....ggagactctctctcgctcg 177

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA:*

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- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	14	7.9	24	2	US-08-609-426A-12	Sequence 12, Appl
4	14	7.9	25	4	US-09-396-196G-63347	Sequence 63347, A
5	14	7.9	25	4	US-09-396-196G-67734	Sequence 67734, A
6	14	7.9	25	4	US-09-396-196G-72314	Sequence 72314, A
7	14	7.9	25	4	US-09-396-196G-106361	Sequence 106361, A
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9	14	7.9	33	1	US-08-151-574-35	Sequence 35, Appl
10	14	7.9	33	1	US-08-146-422-2	Sequence 2, Appl
11	14	7.9	33	1	US-08-146-424-2	Sequence 2, Appl
12	14	7.9	33	1	US-08-626-554-18	Sequence 18, Appl
13	14	7.9	33	1	US-08-693-709-16	Sequence 16, Appl
14	14	7.9	33	1	US-08-638-448-2	Sequence 35, Appl
15	14	7.9	33	1	US-08-419-448-35	Sequence 35, Appl
16	14	7.9	33	3	US-09-233-510-35	Sequence 35, Appl
17	14	7.9	18	3	US-09-344-579-18	Sequence 18, Appl
18	14	7.9	18	3	US-08-961-810-96	Sequence 96, Appl
19	14	7.9	18	3	US-08-353-902D-96	Sequence 96, Appl
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23	14	7.9	20	3	US-08-943-731-527	Sequence 527, Appl
24	14	7.9	20	3	US-09-506-073-73	Sequence 73, Appl
25	14	7.9	20	4	US-09-198-452A-5828	Sequence 5828, Ap
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27	14	7.9	25	4	US-09-396-196G-14024	Sequence 14024, A

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C 33	13	7.3	25	4	US-09-396-196G-63348	Sequence 63348, A
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C 36	13	7.3	25	4	US-09-396-196G-93415	Sequence 93415, A
C 37	13	7.3	25	4	US-09-396-196G-93417	Sequence 93417, A
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C 40	13	7.3	25	4	US-09-396-196G-126870	Sequence 126870, A
C 41	13	7.3	25	5	PCT-US91-03680-155	Sequence 155, App
C 42	13	7.3	25	5	PCT-US91-03680-156	Sequence 156, App
C 43	13	7.3	25	5	PCT-US91-03680-157	Sequence 157, App
C 44	13	7.3	25	5	PCT-US91-03680-158	Sequence 158, App
C 45	13	7.3	40	1	US-08-445-640-18	Sequence 18, Appl
C 46	13	7.3	40	3	US-08-170-558-18	Sequence 18, Appl
C 47	13	7.3	40	3	US-08-447-314-18	Sequence 18, Appl
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C 49	13	7.3	40	4	US-09-223-490-18	Sequence 18, Appl
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C 56	12	6.8	18	3	US-08-488-214A-70	Sequence 70, Appl
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C 63	12	6.8	20	2	US-09-422-978-8223	Sequence 8223, Ap
C 64	12	6.8	20	3	US-08-837-201C-99	Sequence 99, Appl
C 65	12	6.8	20	3	US-09-364-416-99	Sequence 99, Appl
C 66	12	6.8	20	4	US-09-702-251-82	Sequence 82, Appl
C 67	12	6.8	20	4	US-09-568-407-6	Sequence 6, Appl
C 68	12	6.8	20	4	US-09-198-452A-3627	Sequence 3627, Ap
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C 70	12	6.8	20	4	US-09-112-580-211	Sequence 211, Ap
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C 72	12	6.8	21	3	US-08-647-351B-3	Sequence 3, Appl
C 73	12	6.8	21	3	US-09-099-749-7	Sequence 7, Appl
C 74	12	6.8	21	3	US-09-326-074-3	Sequence 3, Appl
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C 77	12	6.8	22	3	US-09-569-601A-21	Sequence 21, Appl
C 78	12	6.8	22	3	US-08-765-332-28	Sequence 28, Appl
C 79	12	6.8	22	3	US-09-041-886-64	Sequence 64, Appl
C 80	12	6.8	22	3	US-09-448-894-28	Sequence 28, Appl
C 81	12	6.8	22	4	US-09-931-486-28	Sequence 28, Appl
C 82	12	6.8	24	4	US-09-044-604-8	Sequence 8, Appl
C 83	12	6.8	24	4	US-09-382-552-173	Sequence 173, App
C 84	12	6.8	25	1	US-08-197-811-4	Sequence 4, Appl
C 85	12	6.8	25	2	US-08-468-042C-4	Sequence 4, Appl
C 86	12	6.8	25	3	US-08-748-130-29	Sequence 29, Appl
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C 89	12	6.8	25	4	US-09-396-196G-24647	Sequence 24647, A
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C 92	12	6.8	25	4	US-09-396-196G-52582	Sequence 52582, A
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C 97	12	6.8	25	4	US-09-396-196G-87318	Sequence 87318, A
C 98	12	6.8	25	4	US-09-396-196G-87318	Sequence 87318, A
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C 100	12	6.8	25	4	US-09-396-196G-92011	Sequence 92011, A
C 100	12	6.8	25	4	US-09-396-196G-92012	Sequence 92012, A

ALIGNMENTS

```
RESULT 1
US-09-693-555A-13
Sequence 13, Application US/09693555A
Patent No. 6733967
GENERAL INFORMATION:
APPLICANT: KORNMAN, KENNETH
APPLICANT: DUFF, GORDON
APPLICANT: OFFENBACHER, STEVEN
TITLE OF INVENTION: FERTIL TESTING FOR PREDICTION OF LOW BIRTH WEIGHT
FILE REFERENCE: MSA-009.01
CURRENT APPLICATION NUMBER: US/09/693,555A
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: PCT/US99/08794
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/082,487
PRIOR FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-693-555A-13

Query Match
Best Local Similarity 100.0%; Score 14; DB 4; Length 23;
Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

118 GAAGCCCTCCCG 131
118 GAAGCCCTCCCG 14
Db

RESULT 2
US-07-923-724-12/c
Sequence 12, Application US/07923724
Patent No. 5780292
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
US-07-923-724-12

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 24;
Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

51 CTCGACCGACGACCG 64
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Db
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RESULT 3
US-08-609-426A-12/c
Sequence 12, Application US/08609426A
Patent No. 5830733
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 1231.12 Seconds
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5472.564 Million cell updates/sec

Title: US-09-887-941B-3

Perfect score: 177
Sequence: 1 gcttcctttctcgcgttc.....ggagactgcctcctcgcctcg 177

Scoring table: OLIGO_NUC
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Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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7	13	7.3	33	4	BI829654 603079396
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47	12	6.8	36	4	BI811125 SALK_0574
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79	12	6.8	36	4	BI811125 SALK_0574
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33	12	6.8	46	1	AA717367
34	12	6.8	47	8	AZ852673
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36	12	6.8	50	1	AUI05546
37	12	6.8	50	6	CD532122
38	12	6.8	50	8	AZ510728
39	12	6.8	50	9	BI821751
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98 11 6.2 39 4 BU065029 BU065029
 99 11 6.2 39 9 AG202285 AG202285 Pen trogl
 100 11 6.2 39 9 AL943780 AL943780 Arabidops

ALIGNMENTS

RESULT 1
 LOCUS AI955350 37 bp mRNA EST 19-AUG-1999
 DEFINITION wcl1d12.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2507159 3'

similar to SW:MLH1_HUMAN P40692 MUTL PROTEIN HOMOLOG 1 ; mRNA
 sequence.

ACCESSION AI955350 GI:5747660
 VERSION AI955350.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 37)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality
 Seg primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source

1..37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2507159"
 /tissue_type="well-differentiated endometrial
 adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Utl1"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN

Query Match 7.3%; Score 14; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 CTCGATCTTTGGA 97
 |||||
 10 CTCGATCTTTGGA 23

RESULT 2
 LOCUS BI762555/c 32 bp mRNA linear EST 25-SEP-2001
 DEFINITION 60304865f1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188724 5',
 mRNA sequence.
 ACCESSION BI762555
 VERSION BI762555.1 GI:15754133
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 32)

NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11471 row: j column: 21
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES
 source

1..32
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5188724"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC library."

ORIGIN

Query Match 7.3%; Score 13; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 TGCCCTCATCTTT 93
 |||||
 14 TGCCCTCATCTTT 2

RESULT 3

BI832949/c 32 bp mRNA linear EST 04-OCT-2001
 LOCUS 60309078f1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5229556 5',
 mRNA sequence.

ACCESSION BI832949
 VERSION BI832949.1 GI:15944499
 EST.

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 32)

NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 186.129 seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-3

Perfect score: 177
Sequence: 1 gcttcctttctcgcgttc.....gggactgctcctcgcctcg 177

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

N_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	9.0	32	8	AA550042 Human F1d
2	15	8.5	18	8	ABX10978 Human Zep
3	14	7.9	17	8	ADA99413 Human MDZ
4	14	7.9	17	8	ADA99411 Human MDZ
5	14	7.9	17	8	ADA99412 Human MDZ
6	14	7.9	17	8	ADA99410 Human MDZ
7	14	7.9	20	10	ACF79692 Sense prt
8	14	7.9	23	3	AA237214 PCR prime
9	14	7.9	23	3	AA63789 Human TNF
10	14	7.9	23	6	AA27403 Human tum
11	14	7.9	24	2	AA058130 chhl-Phyt
12	14	7.9	24	6	AA032967 Pear beta
13	14	7.9	25	8	ADB00914 Human MDZ
14	14	7.9	25	8	ADB00921 Human MDZ
15	14	7.9	25	8	ADB00911 Human MDZ
16	14	7.9	25	8	ADB00919 Human MDZ
17	14	7.9	25	8	ADB00913 Human MDZ
18	14	7.9	25	8	ADB00915 Human MDZ
19	14	7.9	25	8	ADB00918 Human MDZ
20	14	7.9	25	8	ADB00912 Human MDZ

21	14	7.9	25	8	ADB00920 Human MDZ
22	14	7.9	25	8	ADB00917 Human MDZ
23	14	7.9	25	8	ADB00910 Human MDZ
24	14	7.9	25	8	ADB00916 Human MDZ
25	14	7.9	25	9	ACK10775 Human mic
26	14	7.9	26	3	AA251522 Control e
27	14	7.9	26	6	AA140163 Isoprenol
28	14	7.9	26	12	AD007948 Antisense
29	14	7.9	29	13	ADR32545 Human nic
30	14	7.9	33	2	AA651845 Phytase g
31	14	7.9	33	2	AA61882 A. niger
32	14	7.9	35	3	AA63569 MiniSeqe
33	14	7.9	50	4	AA130967 Human SNP
34	13	7.3	15	2	AA52877 Adenosine
35	13	7.3	15	3	AA333321 A3 adenos
36	13	7.3	15	3	AA03715 Human ade
37	13	7.3	15	3	AA18442 Human ade
38	13	7.3	15	3	AA99534 Adenosine
39	13	7.3	15	4	AA46398 IGFBP2 o1
40	13	7.3	15	4	AA46397 IGFBP2 o1
41	13	7.3	15	4	AA46399 IGFBP2 o1
42	13	7.3	15	10	AB294136 Human pho
43	13	7.3	15	11	ABD32528 Al/A3 ant
44	13	7.3	17	4	ABA80224 MLH1 muta
45	13	7.3	17	4	ABA80225 MLH1 muta
46	13	7.3	17	8	ADA99414 Human MDZ
47	13	7.3	17	8	ADA99409 Human MDZ
48	13	7.3	17	10	AD150192 Human tum
49	13	7.3	18	2	AA090905- Human Ets
50	13	7.3	18	3	AA338359 Human Ets
51	13	7.3	18	3	AA672228 Single nu
52	13	7.3	18	4	AA26538 Human pro
53	13	7.3	19	2	AA76054 Human N1p
54	13	7.3	19	11	AD170053 Human GIP
55	13	7.3	19	11	AD169940 Human GIP
56	13	7.3	19	12	ADH01541 Protein t
57	13	7.3	19	12	ADH01477 Human pro
58	13	7.3	19	12	ADH01476 Human pro
59	13	7.3	19	12	ADH01614 Protein t
60	13	7.3	19	12	ADN75743 PRPB ass
61	13	7.3	19	12	ADN75742 PRPB ass
62	13	7.3	20	2	AA087113 Aspergill
63	13	7.3	20	2	AA96502 PCR prime
64	13	7.3	20	5	AA522295 Human COL
65	13	7.3	20	6	AB145285 Human chr
66	13	7.3	20	6	AAAD4828 Human raf
67	13	7.3	20	6	AB197537 Capture o
68	13	7.3	20	8	ADA00937 Human Ras
69	13	7.3	20	9	AB744394 ChimERIC
70	13	7.3	20	10	ACD42144 Human raf
71	13	7.3	21	4	AA54504 Primer fo
72	13	7.3	21	10	ACF79746 Human ant
73	13	7.3	21	12	ADH01478 Human pro
74	13	7.3	21	12	ADH01475 Human pro
75	13	7.3	21	12	ADH01479 Human pro
76	13	7.3	21	12	ADN75745 PRPB ass
77	13	7.3	21	12	ADN75744 PRPB ass
78	13	7.3	21	12	ADN75741 Human prp
79	13	7.3	23	3	AA287370 Hepatitis
80	13	7.3	24	6	AB191644 Capture o
81	13	7.3	24	6	AB191645 Capture o
82	13	7.3	25	8	ADB00922 Human MDZ
83	13	7.3	25	8	ADB00909 Human MDZ
84	13	7.3	25	9	ACK17044 Human mic
85	13	7.3	25	9	ACK19756 Human mic
86	13	7.3	25	9	ACK25519 Human mic
87	13	7.3	25	9	ACK25519 Human mic
88	13	7.3	27	6	AA140165 Isoprenol
89	13	7.3	29	8	AB083220 Coffee Rb
90	13	7.3	29	12	ADP18514 Synthetic
91	13	7.3	31	4	AA131001 Human sin
92	13	7.3	33	10	ACC49803 Human myo
93	13	7.3	35	10	ADC35659 Dehydroge

94	13	7.3	40	2	AAQ94428	Human Rae
95	13	7.3	40	13	ADR50610	Ad50610 PCR prime
96	13	7.3	41	2	AAV47770	AAV47770 Maize pol
97	13	7.3	41	2	AAV47771	AAV47771 Maize pol
98	13	7.3	41	6	ABL40992	ABL40992 Homo DNA
99	13	7.3	41	6	ABZ45216	ABZ45216 Human ATP
100	13	7.3	41	6	ABZ49628	ABZ49628 Human sul

ALIGNMENTS

RESULT 1

AADS0042 standard; DNA; 32 BP.

AC AADS0042; (first entry)

DT 24-MAR-2003

Human fldnaMAPKAP-2 CDNA cloning PCR primer #5.

Human; mitogen-activated protein kinase activating protein kinase-2; MAPKAP-2 kinase; signal transduction; cell proliferative disorder; immune system disorder; inflammation; arthritis; immunomodulator; cytostatic; gene therapy; PCR; primer; ss.

Homo sapiens.

WO200230524-A2.

14-NOV-2002.

25-FEB-2002; 2002WO-US005670.

28-FEB-2001; 2001US-0272260P.

(MERI) MERCK & CO INC.

Lograsso P, Hawkins J, Lisnack JM;

WPI; 2003-111970/10.

New isolated nucleic acid molecule encoding a human mitogen-activated protein kinase activating protein kinase-2 (MAPKAP-2), useful for treating immune-system related disorders, inflammation and arthritis.

Example 1; Page 124; 150pp; English.

The invention relates to an isolated nucleic acid molecule comprising a sequence of nucleotides that encode a human mitogen-activated protein kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region that encodes a splice variant of a MAPKAP-2 kinase. The invention is especially useful in regulating signal transduction in a cell and in disorders, immune system disorders, inflammation, arthritis. The nucleic acid and the polypeptide may also be used in screening assays, predictive medicine, diagnostic or prognostic assays, chromosome mapping, tissue typing, pharmacogenomics and in monitoring clinical trials. The invention is useful in gene therapy. The present sequence is human full length MAPKAP-2 kinase, fldnaMAPKAP-2 CDNA cloning PCR primer

Sequence 32 BP; 5 A; 15 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 9.0%; Score 16; DB 8; Length 32;

Best Local Similarity 100.0%; Pred. No. 9.9e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 10 CCCTCCAGGCGCAG 25

94	13	7.3	40	2	AAQ94428	Human Rae
95	13	7.3	40	13	ADR50610	Ad50610 PCR prime
96	13	7.3	41	2	AAV47770	AAV47770 Maize pol
97	13	7.3	41	2	AAV47771	AAV47771 Maize pol
98	13	7.3	41	6	ABL40992	ABL40992 Homo DNA
99	13	7.3	41	6	ABZ45216	ABZ45216 Human ATP
100	13	7.3	41	6	ABZ49628	ABZ49628 Human sul

RESULT 2

ABX10978/c

ABX10978 standard; DNA; 18 BP.

ABX10978;

17-AUG-2003 (first entry)

Human Zepm1 gene specific PCR primer ZC17, 822.

Human; PCR; ss; Zepm1; epithelial morphogenesis; dermatological; vulnary; endocrine; gene therapy; protein transport; primer; neurotransmission; epithelial morphogenesis; epithelial cell disorder; alopecia; chromosomal mapping.

Homo sapiens.

US2003032778-A1.

13-FEB-2003.

26-FEB-2002; 2002US-00085188.

14-DEC-1998; 98US-0112246P.

13-DEC-1999; 99US-00459544.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Taft DW;

WPI; 2003-466250/44.

New isolated polypeptide from the human syntaxin/epimorphin family, designated as Zepm1, useful in protein transport, neurotransmission, and epithelial morphogenesis for treating epithelial cell disorders, such as alopecia.

Example 2; Page 33; 39pp; English.

This invention relates to a novel polypeptide, designated Zepm1 which is capable of effecting epithelial morphogenesis. The invention also comprises an expression vector comprising the Zepm1 nucleic acid molecule, a method for producing the human Zepm1 protein of the invention, and a method for detecting the presence of Zepm1 or Zepm1 RNA in a biological sample. The DNA and protein sequences of the invention may have dermatological, vulnary or endocrine activities and may be used in gene therapy. The polypeptides, nucleic acid molecules and methods of the invention are useful in protein transport, neurotransmission, and epithelial morphogenesis, particularly for treating epithelial cell disorders, such as alopecia. The present sequence represents a PCR primer specific for the human Zepm1 DNA sequence of the invention, this PCR primer was used with the primer shown in ABX10979 to map the chromosomal location of the human Zepm1 gene

Sequence 18 BP; 2 A; 2 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 15; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 50 TCTCCACGACGCG 64

18 TCTCCACGACGCG 4

RESULT 3

ADA99413 standard; DNA; 17 BP.

ADA99413;

20-NOV-2003 (first entry)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1086.04 Seconds
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Title: US-09-887-941b-3

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 399 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers

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 VERSION AX687668.1 GI:29410364
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 400 05-FEB-2003;
 Aeomica, Inc. (US)
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 VERSION AX687669.1 GI:29410365
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 401 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers

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 DEFINITION Sequence 402 from Patent EP1281758.
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 VERSION AX687670.1 GI:29410366
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 402 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers

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QY 19 TTCTCTCACTATCCT 32
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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4536.068 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 206499, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:

APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 206499
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-206499

Query Match 8.1%; Score 25; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 GGCTACGATGAGTACATGACGGGC 174
DB 25 GGCTACGATGAGTACATGACGGGC 1

RESULT 2
US-10-956-157-214615/c
Sequence 214615, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 214615
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-214615

Query Match 8.1%; Score 25; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 GCAAGTGTCCAGCTGCTGCATGTC 227
DB 25 GCAAGTGTCCAGCTGCTGCATGTC 1

RESULT 3
US-10-956-157-201630/c
Sequence 201630, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 201630
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-201630

Query Match 7.5%; Score 23; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ACCAGACATTCACGCCGGTGG 100
DB 23 ACCAGACATTCACGCCGGTGG 1

RESULT 4
US-11-036-317-214871/c
Sequence 214871, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIORITY FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 214871
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-214871

Query Match 6.2%; Score 19; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7%;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GCAGCAGCAGCAGCAGCA 194
DB 23 GCAGCAGCAGCAGCAGCA 5

RESULT 5
US-11-036-317-227382
Sequence 227382, Application US/11036317
Publication No. US20050214823A1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-887-941B-2

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA: *
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5: /cgm2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgm2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	5.5	21	2	US-08-267-803B-66
5	17	5.5	21	2	US-08-863-639A-28
6	17	5.5	21	2	US-08-863-639A-40
7	17	5.5	21	2	US-08-863-639A-60
8	17	5.5	21	2	US-08-863-639A-66
9	17	5.5	21	2	US-08-863-639A-69
10	17	5.5	21	2	US-08-863-639A-87
11	17	5.5	24	2	US-08-863-639A-94
12	17	5.5	25	4	US-09-396-196G-74107
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14	17	5.5	30	1	US-08-068-747-11
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19	17	5.5	31	5	PCT-US95-02861-14
20	17	5.5	33	2	US-08-863-639A-29
21	17	5.5	33	4	US-09-475-947A-251
22	17	5.5	36	2	US-08-863-639A-31
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C 29	16	5.2	43	3	US-08-732-708C-10	Sequence 10, Appli
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C 31	16	5.2	50	3	US-09-422-936-22	Sequence 22, Appli
C 32	16	5.2	50	3	US-09-422-936-62	Sequence 62, Appli
C 33	15	4.9	18	3	US-09-487-444-11	Sequence 11, Appli
C 34	15	4.9	21	3	US-08-628-540-8	Sequence 8, Appli
C 35	15	4.9	21	3	US-08-628-540-9	Sequence 9, Appli
C 36	15	4.9	21	3	US-08-941-100-3	Sequence 3, Appli
C 37	15	4.9	21	3	US-08-941-100-4	Sequence 4, Appli
C 38	15	4.9	25	4	US-09-396-196G-2490	Sequence 2490, Ap
C 39	15	4.9	25	4	US-09-396-196G-5126	Sequence 5126, Ap
C 40	15	4.9	25	4	US-09-396-196G-50623	Sequence 50623, A
C 41	15	4.9	25	4	US-09-396-196G-115504	Sequence 115504,
C 42	15	4.9	34	3	US-08-968-563-46	Sequence 46, Appli
C 43	15	4.9	34	3	US-08-969-683A-46	Sequence 46, Appli
C 44	15	4.9	34	3	US-08-297-928-18	Sequence 18, Appli
C 45	15	4.9	34	4	US-09-641-652-24	Sequence 24, Appli
C 46	15	4.9	39	2	US-08-533-298-16	Sequence 16, Appli
C 47	15	4.9	39	2	US-08-533-298-18	Sequence 18, Appli
C 48	15	4.9	39	3	US-08-721-458B-67	Sequence 67, Appli
C 49	15	4.9	41	3	US-08-721-458B-68	Sequence 68, Appli
C 50	15	4.9	45	3	US-08-721-458B-62	Sequence 62, Appli
C 51	15	4.9	47	3	US-09-641-638-877	Sequence 877, App
C 52	15	4.9	47	3	US-09-641-638-878	Sequence 877, App
C 53	15	4.9	47	4	US-10-170-097-877	Sequence 877, App
C 54	15	4.9	47	4	US-10-170-097-878	Sequence 878, App
C 55	14	4.5	15	3	US-09-163-485-13	Sequence 13, Appli
C 56	14	4.5	15	4	US-09-475-947A-304	Sequence 304, App
C 57	14	4.5	18	4	US-09-679-298A-30	Sequence 30, Appli
C 58	14	4.5	20	3	US-09-907-843-23	Sequence 23, Appli
C 59	14	4.5	23	4	US-09-083-268-11	Sequence 11, Appli
C 60	14	4.5	25	4	US-09-396-196G-51515	Sequence 51515, A
C 61	14	4.5	25	4	US-09-396-196G-53525	Sequence 53525, A
C 62	14	4.5	25	4	US-09-396-196G-65285	Sequence 65285, A
C 63	14	4.5	25	4	US-09-396-196G-68127	Sequence 68127, A
C 64	14	4.5	25	4	US-09-396-196G-68128	Sequence 68128, A
C 65	14	4.5	25	4	US-09-396-196G-100855	Sequence 100855,
C 66	14	4.5	25	4	US-09-396-196G-102899	Sequence 102899,
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C 69	14	4.5	25	4	US-09-396-196G-125084	Sequence 125084,
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C 71	14	4.5	35	4	US-09-598-747-32	Sequence 32, Appli
C 72	14	4.5	36	2	US-08-863-639A-18	Sequence 18, Appli
C 73	14	4.5	36	2	US-09-438-268-50	Sequence 50, Appli
C 74	14	4.5	38	2	US-08-857-946-108	Sequence 108, App
C 75	14	4.5	38	3	US-08-970-740-108	Sequence 108, App
C 76	14	4.5	39	3	US-08-444-818-761	Sequence 761, App
C 77	14	4.5	40	1	US-08-399-696-23	Sequence 23, Appli
C 78	14	4.5	47	3	US-09-641-638-876	Sequence 876, App
C 79	14	4.5	47	4	US-10-170-097-876	Sequence 876, App
C 80	13	4.2	15	3	US-09-180-437-104	Sequence 104, App
C 81	13	4.2	18	3	US-09-255-911-31	Sequence 31, Appli
C 82	13	4.2	19	4	US-09-422-978-4399	Sequence 4399, Ap
C 83	13	4.2	20	3	US-09-288-461-27	Sequence 27, Appli
C 84	13	4.2	20	4	US-09-758-881-27	Sequence 27, Appli
C 85	13	4.2	20	4	US-09-899-440-3	Sequence 3, Appli
C 86	13	4.2	22	4	US-09-390-134B-13	Sequence 13, Appli
C 87	13	4.2	23	3	US-09-632-098-24	Sequence 24, Appli
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C 89	13	4.2	25	4	US-09-396-196G-7992	Sequence 7992, Ap
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C 91	13	4.2	25	4	US-09-396-196G-16881	Sequence 16881, A
C 92	13	4.2	25	4	US-09-396-196G-18819	Sequence 18819, A
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C 96	13	4.2	25	4	US-09-396-196G-23457	Sequence 23457, A
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C 98	13	4.2	25	4	US-09-396-196G-65286	Sequence 65286, A
C 99	13	4.2	25	4	US-09-396-196G-72670	Sequence 72670, A
C 100	13	4.2	25	4	US-09-396-196G-72670	Sequence 72670, A

ALIGNMENTS

RESULT 1
US-08-531-927B-17/C
Sequence 17, Application US/08531927B
Patent No. 5840491
GENERAL INFORMATION:
APPLICANT: Kakizuka, Akira
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATH95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-531-927B-17

Query Match 6.8%; Score 21; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 CAGCAGCAGCAGCAGCAGCA 194
DB 42 CAGCAGCAGCAGCAGCAGCA 22

RESULT 2
PCT-US95-06385-7/C
Sequence 7, Application PC/TUS9506385
GENERAL INFORMATION:
APPLICANT: Wei, ET AL.
TITLE OF INVENTION: Transforming Growth Factor Alpha III
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA

ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06385
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NONE
FILING DATE: NONE
ATTORNEY/AGENT INFORMATION:
NAME: PERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-351
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
PCT-US95-06385-7

Query Match 6.5%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 GGCTACGATGAGTCATGA 169
DB 33 GGCTACGATGAGTCATGA 14

RESULT 3
US-08-863-639A-17/C
Sequence 17, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel wordperfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muech
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 17:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 2142.29 Seconds
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5472.564 Million cell updates/sec

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Perfect score: 308
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Word size :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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C	7	17	5.5	46	8	A2828047	A2828047 2M0104N14
C	8	15	4.9	23	7	CF300419	7LEAF--04
C	9	15	4.9	39	8	A2635338	A2635338 1M0491E10
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C	11	15	4.9	50	1	AU105903	AU105903 AU105903
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C	16	14	4.5	50	1	AU103544	AU103544 AU103544
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C	74	12	3.9	50	1	AU105886	AU105886 AU106027
C	75	12	3.9	50	1	AU106027	AU106027 AU106028
C	76	12	3.9	50	1	AU106028	AU106028 AU106807
C	77	12	3.9	50	1	AU106807	AU106807 AU107222
C	78	12	3.9	50	1	AU107222	AU107222 AU107225
C	79	12	3.9	50	1	AU107225	AU107225 OCUC25F04.
C	80	12	3.9	50	6	CP063684	CP063684 SNEStbaa2
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C	82	12	3.9	50	8	AZ575718	AZ575718 AST-733A0
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C	91	11	3.6	21	8	AZ802584	AZ802584 2M0112M01
C	92	11	3.6	21	8	AZ831993	Pan trogus
C	93	11	3.6	21	9	AG301733	AG301733 Arabidops
C	94	11	3.6	22	4	AU590074	AU590074 BM400878
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98 11 3.6 25 9 CG715742 1119043B1
 99 11 3.6 25 9 CG724924 1119083B0
 c 100 11 3.6 26 5 BQ584383 BQ584383 E011859-0

ALIGNMENTS

RESULT 1
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 LOCUS 602054466F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193608 5',
 DEFINITION mRNA sequence.
 BF537767
 ACCESSION BF537767.1 GI:11625135
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 50)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plate: LLM9526 row: c column: 17
 High quality sequence stop: 50.
 Location/Qualifiers

FEATURES
 source 1..50
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4193608"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1ib="NCI CGAP SG2"
 /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1;
 NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo
 dT. Average insert size 1.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 5.8%; Score 18; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 GCAGCAGCAGCAGCAGC 189
 |||||
 Db 30 GCAGCAGCAGCAGCAGC 13

RESULT 2
 A2779573 24 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0016K09 Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG2M0016K09 F, genomic survey sequence.
 ACCESSION A2779573
 VERSION A2779573.1 GI:12910362
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
 JOURNAL Unpublished (2000)
 CONTACT Contact: Robert B. Weiss
 UNIVERSITY University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunne@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0016 row: K column: 09
 SEQ PRIMER: CGTTGTAAACGACGCGCAGT
 CLASS: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES
 source 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0016K09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: pMD29v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI:4732114|9b|AF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 5.5%; Score 17; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 GCAGCAGCAGCAGCAGC 189
 |||||
 Db 1 GCAGCAGCAGCAGCAGC 17

RESULT 3
 A2404206/c 27 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0172120F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG1M0172120 F, genomic survey sequence.
 ACCESSION A2404206
 VERSION A2404206.1 GI:10528219
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 323.886 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-2
Perfect score: 308
Sequence: 1 ctagggttagcgtgctctgtg.....ggaacacagatcgccggggg 308

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

1: Geneseq_16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	6.5	33	2	AA15433 Human tra
2	19	6.2	31	6	AA289256 Human emb
3	19	6.2	36	6	ABA96943 Human den
4	19	6.2	38	4	AA448359 Human FOL
5	19	6.2	45	5	AAH24422 Oligonuc
6	18	5.8	20	3	AAA55806 Human his
7	18	5.8	20	4	AA43116 Antisense
8	18	5.8	20	4	AA89545 Human HDA
9	18	5.8	20	4	AA89536 Human HDA
10	18	5.8	20	10	AB286068 Human o1i
11	18	5.8	20	11	ABD22298 Human sta
12	18	5.8	22	4	AA64183 Human pro
13	18	5.8	22	4	AA64181 Human pro
14	18	5.8	22	5	ACA59989 Prostate
15	18	5.8	22	5	ACA59991 Prostate
16	18	5.8	22	8	ACC95718 Prostate
17	18	5.8	22	8	ACC95716 Prostate
18	18	5.8	22	10	ADB14387 Human pro
19	18	5.8	22	10	ADB14385 Human pro
20	18	5.8	22	10	ADG26801 Human pro

21	18	5.8	22	10	ADG26803	ADG26803 Human pro
22	18	5.8	30	3	AA289258	AA289258 Human emb
23	18	5.8	31	4	AA129930	AA129930 Human sin
24	18	5.8	39	2	AA185359	AA185359 Spider si
25	18	5.8	39	2	AA185336	AA185336 Spider si
26	18	5.8	39	2	AA185358	AA185358 Spider si
27	18	5.8	39	2	AA185357	AA185357 Spider si
28	18	5.8	44	2	AAV68379	AAV68379 Clone #5
29	18	5.8	50	2	AAV68378	AAV68378 Clone #4
30	17	5.5	18	4	AA13717	AA13717 Simple se
31	17	5.5	18	12	ADN97239	ADN97239 Primer of
32	17	5.5	18	12	ADN97238	ADN97238 Synthetic
33	17	5.5	18	12	ADN97237	ADN97237 Synthetic
34	17	5.5	18	12	ADN97236	ADN97236 Synthetic
35	17	5.5	18	12	ADN97235	ADN97235 Synthetic
36	17	5.5	18	12	ADN97234	ADN97234 Synthetic
37	17	5.5	18	13	ADN97233	ADN97233 Allele A
38	17	5.5	20	6	ADN97232	ADN97232 Allele A
39	17	5.5	20	10	ADN97231	ADN97231 Human MEK
40	17	5.5	20	10	ADN97230	ADN97230 Human MEK
41	17	5.5	20	10	ADN97229	ADN97229 Human MEK
42	17	5.5	20	11	ADN97228	ADN97228 Human MEK
43	17	5.5	21	3	AA15433	AA15433 Human tra
44	17	5.5	21	4	AA15432	AA15432 Human tra
45	17	5.5	21	4	AA15431	AA15431 Human tra
46	17	5.5	21	6	AA15430	AA15430 Human tra
47	17	5.5	21	6	AA15429	AA15429 Human tra
48	17	5.5	21	6	AA15428	AA15428 Human tra
49	17	5.5	21	9	AA15427	AA15427 Human tra
50	17	5.5	22	3	AA15426	AA15426 Human tra
51	17	5.5	23	10	AA15425	AA15425 Human tra
52	17	5.5	24	6	AA15424	AA15424 Human tra
53	17	5.5	24	6	AA15423	AA15423 Human tra
54	17	5.5	24	8	AA15422	AA15422 Human tra
55	17	5.5	24	10	AA15421	AA15421 Human tra
56	17	5.5	24	12	AA15420	AA15420 Human tra
57	17	5.5	24	12	AA15419	AA15419 Human tra
58	17	5.5	24	13	AA15418	AA15418 Human tra
59	17	5.5	25	2	AA15417	AA15417 Human tra
60	17	5.5	25	8	AA15416	AA15416 Human tra
61	17	5.5	25	8	AA15415	AA15415 Human tra
62	17	5.5	26	13	AA15414	AA15414 Human tra
63	17	5.5	27	12	AA15413	AA15413 Human tra
64	17	5.5	29	2	AA15412	AA15412 Human tra
65	17	5.5	30	3	AA15411	AA15411 Human tra
66	17	5.5	30	4	AA15410	AA15410 Human tra
67	17	5.5	30	4	AA15409	AA15409 Human tra
68	17	5.5	31	2	AA15408	AA15408 Human tra
69	17	5.5	31	2	AA15407	AA15407 Human tra
70	17	5.5	31	2	AA15406	AA15406 Human tra
71	17	5.5	31	4	AA15405	AA15405 Human tra
72	17	5.5	33	2	AA15404	AA15404 Human tra
73	17	5.5	33	6	AA15403	AA15403 Human tra
74	17	5.5	33	6	AA15402	AA15402 Human tra
75	17	5.5	33	8	AA15401	AA15401 Human tra
76	17	5.5	33	10	AA15400	AA15400 Human tra
77	17	5.5	35	3	AA15399	AA15399 Human tra
78	17	5.5	36	2	AA15398	AA15398 Human tra
79	17	5.5	37	2	AA15397	AA15397 Human tra
80	17	5.5	37	12	AA15396	AA15396 Human tra
81	17	5.5	38	2	AA15395	AA15395 Human tra
82	17	5.5	38	2	AA15394	AA15394 Human tra
83	17	5.5	38	10	AA15393	AA15393 Human tra
84	17	5.5	38	10	AA15392	AA15392 Human tra
85	17	5.5	38	12	AA15391	AA15391 Human tra
86	17	5.5	39	2	AA15390	AA15390 Human tra
87	17	5.5	39	4	AA15389	AA15389 Human tra
88	17	5.5	39	4	AA15388	AA15388 Human tra
89	17	5.5	39	12	AA15387	AA15387 Human tra
90	17	5.5	40	2	AA15386	AA15386 Human tra
91	17	5.5	40	4	AA15385	AA15385 Human tra
92	17	5.5	40	4	AA15384	AA15384 Human tra
93	17	5.5	40	5	AA15383	AA15383 Human tra

```
C 94      17      5.5      40      6      AAD33976 PCR prime
C 95      17      5.5      40      8      Abx97712 Human sec
C 96      17      5.5      40      8      ACA93223 Human sec
C 97      17      5.5      40      10     Adf73214 Paramyxov
          98      17      5.5      40      12     ADf55163 Solid sta
          99      17      5.5      41      2     AAV39671 Solid sta
          100     17      5.5      41      4     AbK98808 Solid sta
```

ALIGNMENTS

```
RESULT 1
AA45433/c
ID AA45433 standard; cDNA; 33 BP.
```

```
AC AAT45433;
XX
XX 30-JUL-1997 (first entry)
```

```
DE Human transforming growth factor alpha HII PCR primer.
```

```
KW TGFalpha-HII; AIDS; dementia; ocular disease; kidney disorder;
KW liver disorder; hair follicle development; angiogenesis; ulcer;
KW corneal incision; embryogenesis; gene therapy; neoplasia; psoriasis;
KW polymerase chain reaction; ss.
```

```
OS Synthetic.
```

```
PN WO9636709-A1.
```

```
PD 21-NOV-1996.
```

```
XX 19-MAY-1995; 95WO-US006386.
```

```
XX 19-MAY-1995; 95WO-US006386.
```

```
XX (HUMA-) HUMAN GENOME SCI INC.
```

```
XX Wei Y, Meissner PS, Ni J;
```

```
XX WPI; 1997-012084/01.
```

```
PT Nucleic acid encoding human transforming growth factor-alpha HII - useful
PT for treating, e.g. ocular diseases, kidney and liver disorders, or to
PT stimulate wound healing etc.
```

```
PS Example 2; Page 40; 73pp; English.
```

```
XX The present sequence encodes the PCR primer for amplifying human
XX transforming growth factor alpha HII (TGFalpha-HII), the construct starts
XX at nucleotide 402 and ends at nucleotide 1248. Human TGFalpha-HII can be
XX used to stimulate wound healing; to restore normal neurological
XX functioning after trauma or AIDS; dementia; to treat ocular diseases,
XX kidney and liver disorders; promote hair follicle development; to
XX stimulate angiogenesis for treating burns, ulcers, corneal incisions; and
XX to stimulate embryogenesis. The TGFalpha-HII can be used directly or is
XX generated in situ, i.e. by gene therapy. Antagonists of TGFalpha-HII are
XX useful for treating neoplasia and for treating certain skin disorders,
XX such as psoriasis. Detecting mutations in the polynucleotide sequence is
XX used for diagnosing diseases (or susceptibility to diseases) which result
XX from underexpression of TGFalpha-HII
```

```
XX Sequence 33 BP; 6 A; 13 C; 7 G; 7 T; 0 U; 0 Other;
```

```
Query Match 6.5%; Score 20; DB 2; Length 33;
```

```
Best Local Similarity 100.0%; Pred. No. 8.5;
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 150 GGCTACGATGAGTACATGA 169
DB 33 GGCTACGATGAGTACATGA 14
```

```
RESULT 2
AAZ89256/c
ID AAZ89256 standard; DNA; 31 BP.
```

```
AC AAZ89256;
```

```
XX 09-JUN-2000 (first entry)
```

```
DE Human embryonic brain protein PCR primer #1.
```

```
KW Human; brain; nerve degeneration; neurotropic; neuroprotective;
KW anticonvulsant; antiparkinsonian; antidiabetic; treatment; infarction;
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;
KW macular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
KW ss.
```

```
OS Homo sapiens.
```

```
PN WO200007614-A1.
```

```
PD 17-FEB-2000.
```

```
XX 02-AUG-1999; 99WO-JP004171.
```

```
XX 05-AUG-1998; 98JP-0022186.
```

```
XX 05-FEB-1999; 99JP-00029164.
```

```
XX (SAKA ) OTSUKA PHARM CO LTD.
```

```
XX Horie M, Hirano H, Kushiki H, Mitsumoto Y, Mori A, Watanabe A;
```

```
XX WPI; 2000-205568/18.
```

```
PT New protein isolated from human embryonic brain useful for treating nerve
PT degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
```

```
PS Example 2; Page 61; 69pp; Japanese.
```

```
XX This invention describes a novel human embryonic brain derived protein
XX (I) which has neurotropic, neuroprotective, anticonvulsant,
XX antiparkinsonian and antidiabetic activity. (I) is useful for treating
XX nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's
XX disease, muscular hypoplastic lateral sclerosis, Huntington's disease,
XX brain infarction, diabetic neuropathy and traumatic nerve degeneration.
XX AAZ89256-289234 represent PCR primers used in the isolation and
XX amplification of the human brain protein described in the method of the
XX invention
```

```
XX Sequence 31 BP; 4 A; 11 C; 9 G; 7 T; 0 U; 0 Other;
```

```
Query Match 6.2%; Score 19; DB 3; Length 31;
```

```
Best Local Similarity 100.0%; Pred. No. 27;
```

```
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 132 AGCGAGCTTCACCGGCGG 150
DB 28 AGCGAGCTTCACCGGCGG 10
```

```
RESULT 3
```

```
ABA96943/c
ID ABA96943 standard; DNA; 36 BP.
```

```
XX ABA96943;
```

```
XX 20-MAY-2002 (first entry)
```

```
DE Human dendritic cell membrane protein Siglec-9 sense RT-PCR primer.
```

```
KW Human; Siglec-9; membrane protein; dendritic cell; DC;
KW sialic acid binding immunoglobulin-like lectin 9; anti-Siglec-9 antibody;
KW cancer; vaccine; immunotherapy; reverse transcription-PCR; RT-PCR;
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1889.83 Seconds
(without alignments)
7697.122 Million cell updates/sec

Title: US-09-887-941b-2

Perfect score: 308
Sequence: 1 ctgagggtaggctgtctgtcgtg.....ggacacagatcgcg9999 308

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ha:*
2: gb_hctg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_vn:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	6.8	43	6	AR059527 Sequence
C 2	19	6.2	31	6	E37925
C 3	19	6.2	36	6	BD095049 Antibody
C 4	19	6.2	45	6	E59414
C 5	18	5.8	20	6	BD244919
C 6	18	5.8	20	6	AX053082 Sequence
C 7	18	5.8	20	6	AX053091 Sequence
C 8	18	5.8	20	6	AX546302 Sequence
C 9	18	5.8	20	6	AX546332 Sequence
C 10	18	5.8	22	6	AX267961 Sequence
C 11	18	5.8	22	6	AX267963 Sequence
C 12	18	5.8	30	6	E37927
C 13	17	5.5	18	6	AR084528
C 14	17	5.5	18	6	AX598368
C 15	17	5.5	21	6	AR053160
C 16	17	5.5	21	6	AR084539
C 17	17	5.5	21	6	AR084551
C 18	17	5.5	21	6	AR084571
C 19	17	5.5	21	6	AR084577

C 20	17	5.5	21	6	AR084580	AR084580 Sequence
C 21	17	5.5	21	6	AR084598	AR084598 Sequence
C 22	17	5.5	21	6	AX104588	AX104588 Sequence
C 23	17	5.5	21	6	AX355212	AX355212 Sequence
C 24	17	5.5	21	6	AX547641	AX547641 Sequence
C 25	17	5.5	23	6	AX926737	AX926737 Sequence
C 26	17	5.5	24	6	AR084605	AR084605 Sequence
C 27	17	5.5	24	6	BD169605	BD169605 Novel G P
C 28	17	5.5	24	6	BD182475	BD182475 Screening
C 29	17	5.5	24	6	BD102725	BD102725 Ligand fo
C 30	17	5.5	25	6	A27143	A27143 Synthetic 1
C 31	17	5.5	25	6	A27144	A27144 Synthetic 1
C 32	17	5.5	30	6	AR084541	AR084541 Sequence
C 33	17	5.5	30	6	AR165925	AR165925 Sequence
C 34	17	5.5	30	6	E34522	E34522 SCA7 gene a
C 35	17	5.5	30	6	I84405	I84405 Sequence 6
C 36	17	5.5	30	6	I84410	I84410 Sequence 11
C 37	17	5.5	30	6	AX614111	AX614111 Sequence
C 38	17	5.5	31	6	AR078304	AR078304 Sequence
C 39	17	5.5	31	6	AR084540	AR084540 Sequence
C 40	17	5.5	33	6	BD177544	BD177544 Method fo
C 41	17	5.5	33	6	AR241963	AR241963 Sequence
C 42	17	5.5	36	6	A62704	A62704 Sequence 5
C 43	17	5.5	36	6	AR084542	AR084542 Sequence
C 44	17	5.5	37	6	AX328688	AX328688 Sequence
C 45	17	5.5	37	6	BD132253	BD132253 DNA diagn
C 46	17	5.5	38	6	AX328689	AX328689 Sequence
C 47	17	5.5	38	6	BD132254	BD132254 DNA diagn
C 48	17	5.5	39	6	AX328690	AX328690 Sequence
C 49	17	5.5	39	6	BD132255	BD132255 DNA diagn
C 50	17	5.5	40	6	BD175941	BD175941 Paromyxov
C 51	17	5.5	40	6	AR544634	AR544634 Sequence
C 52	17	5.5	40	6	AX328691	AX328691 Sequence
C 53	17	5.5	40	6	BD011782	BD011782 RNP deriv
C 54	17	5.5	40	6	BD132256	BD132256 DNA diagn
C 55	17	5.5	41	6	AX328692	AX328692 Sequence
C 56	17	5.5	41	6	BD132257	BD132257 DNA diagn
C 57	17	5.5	42	6	A62705	A62705 Sequence 6
C 58	17	5.5	42	6	AX328693	AX328693 Sequence
C 59	17	5.5	42	6	BD132258	BD132258 DNA diagn
C 60	17	5.5	43	6	AX328694	AX328694 Sequence
C 61	17	5.5	43	6	BD132259	BD132259 DNA diagn
C 62	17	5.5	44	6	AX328695	AX328695 Sequence
C 63	17	5.5	44	6	BD132260	BD132260 DNA diagn
C 64	17	5.5	45	6	AX328696	AX328696 Sequence
C 65	17	5.5	45	6	BD132261	BD132261 DNA diagn
C 66	17	5.5	46	6	AX328697	AX328697 Sequence
C 67	17	5.5	46	6	BD132262	BD132262 DNA diagn
C 68	17	5.5	47	6	AX328698	AX328698 Sequence
C 69	17	5.5	47	6	BD132263	BD132263 DNA diagn
C 70	17	5.5	48	6	AX328699	AX328699 Sequence
C 71	17	5.5	48	6	BD132264	BD132264 DNA diagn
C 72	17	5.5	49	6	AX167839	AX167839 Sequence
C 73	17	5.5	49	6	AX328700	AX328700 Sequence
C 74	17	5.5	49	6	BD132265	BD132265 DNA diagn
C 75	17	5.5	50	6	C0008695	C0008695 Sequence
C 76	17	5.5	50	6	AX164884	AX164884 Sequence
C 77	17	5.5	50	6	AX190222	AX190222 Sequence
C 78	17	5.5	50	6	AX328701	AX328701 Sequence
C 79	17	5.5	50	6	BD132266	BD132266 DNA diagn
C 80	17	5.5	20	6	AX053083	AX053083 Sequence
C 81	16	5.2	20	6	AX053092	AX053092 Sequence
C 82	16	5.2	20	6	AX488408	AX488408 Sequence
C 83	16	5.2	20	6	AX546303	AX546303 Sequence
C 84	16	5.2	20	6	AX546393	AX546393 Sequence
C 85	16	5.2	22	6	AX360164	AX360164 Sequence
C 86	16	5.2	23	6	AX767321	AX767321 Sequence
C 87	16	5.2	31	6	AR078305	AR078305 Sequence
C 88	16	5.2	34	6	AX328685	AX328685 Sequence
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C 91	16	5.2	35	6	BD132251	BD132251 DNA diagn
C 92	16	5.2	36	6	AX328687	AX328687 Sequence

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ALIGNMENTS

RESULT 1
 LOCUS AR059527/c 43 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 17 from patent US 5840491.
 ACCESSION AR059527
 VERSION AR059527.1 GI:5985977
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Kakiyuka, A.
 TITLE DNA sequence encoding the Machado-Joseph disease gene and uses thereof
 JOURNAL Patent: US 5840491-A 17 24-NOV-1998;
 FEATURES
 source Location/Qualifiers
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 /mol_type="unassigned DNA"

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 DB 42 CAGCAGCAGCAGCAGCAGCA 22

RESULT 2
 LOCUS E37925/c 31 bp DNA linear PAT 31-JAN-2002
 DEFINITION Remedy for diseases with nerve degeneration.
 ACCESSION E37925
 VERSION E37925.1 GI:18624860
 KEYWORDS JP 2000109433-A/3.
 SOURCE JP 2000109433-A/3.
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Horie, M., Hirano, N., Kyushiki, H., Mitsumoto, Y., Mori, A. and Watabe, A.
 TITLE Remedy for diseases with nerve degeneration
 JOURNAL Patent: JP 2000109433-A 3 18-APR-2000;
 COMMENT OTSUKA PHARMACEUT CO LTD
 OS Artificial Sequence
 PN JP 2000109433-A/3
 PD 18-APR-2000
 PF 05-FEB-1999 JP 1999029164
 PR MASATO HORIE, NAONOBU HIRANO, HIROYUKI KYUSHIKI, PI YASUHIRO MITSUMOTO,
 PI ATSUSHI MORI, AKIHIRO WATABE
 PC A61K38/00, A61K31/00, A61K31/00, C07K14/52//C12N15/09,
 PC A61K37/02,
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 FT Key Location/Qualifiers
 FT source 1..31

FT Location/Qualifiers
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 AGCGAGCTTCAACCGGCGG 150
 DB 28 AGCGAGCTTCAACCGGCGG 10

RESULT 3
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 DEFINITION Antibody against dendritic cell (DC) membrane molecule, Siglec-9, and DC detection method and DC separation method using it.
 ACCESSION BD095049
 VERSION BD095049.1 GI:22640637
 KEYWORDS JP 2001352977-A/2.
 SOURCE JP 2001352977-A/2.
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Watarai, H. and Yamaguchi, Y.
 TITLE Antibody against dendritic cell (DC) membrane molecule, Siglec-9, and DC detection method and DC separation method using it
 JOURNAL Patent: JP 2001352977-A 2 25-DEC-2001;
 COMMENT KIRIN BREWERY CO LTD
 OS Artificial Sequence
 PN JP 2001352977-A/2
 PD 25-DEC-2001
 PF 12-JUN-2000 JP 2000176187
 PI HIROSHI WATARAI, YASUNORI YAMAGUCHI
 PC C12N15/02, C07K16/18, C12N15/09, C12P21/08, C12Q1/02, G01N33/53, PC G01N33/53
 CC GOIN33/57//C12Q1/68, C12N15/00, C12N15/00
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 CC sequence of Siglec-9 gene
 CC key Location/Qualifiers
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 FT Location/Qualifiers
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ORIGIN

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 DB 21 GGGCAGCAGCAGCAGCAGC 3

RESULT 4
 LOCUS E59414/c 45 bp DNA linear PAT 31-JAN-2002
 DEFINITION Signal peptide.
 ACCESSION E59414
 VERSION E59414.1 GI:18622547
 KEYWORDS JP 2000354490-A/1.
 SOURCE JP 2000354490-A/1.
 ORGANISM synthetic construct
 FT source 1..31

GenCore version 5.1.6
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Run on: October 8, 2005, 04:55:56 ; Search time 813.781 Seconds
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Title: US-09-887-941B-1

Perfect score: 530

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	3.2	25	24	US-11-036-317-79000
5	17	3.2	25	24	US-11-036-317-101784
6	16	3.0	24	17	US-10-401-194-42
7	16	3.0	22	22	US-10-719-956-439303

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C	10	16	3.0	25	24	US-11-036-317-145557	Sequence 145557,
C	11	16	3.0	25	24	US-11-036-317-674408	Sequence 674408,
C	12	16	3.0	25	24	US-11-036-317-726872	Sequence 726872,
C	13	16	3.0	25	24	US-11-036-317-807089	Sequence 807089,
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C	15	16	3.0	47	17	US-10-326-684-853	Sequence 853, App
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C	22	15	2.8	20	21	US-10-719-900-112804	Sequence 12804,
C	23	15	2.8	25	21	US-10-719-900-172512	Sequence 145182,
C	24	15	2.8	25	21	US-10-719-900-318333	Sequence 172532,
C	25	15	2.8	25	21	US-10-719-900-489619	Sequence 318333,
C	26	15	2.8	25	21	US-10-719-900-699095	Sequence 489619,
C	27	15	2.8	25	21	US-10-719-900-710757	Sequence 699095,
C	28	15	2.8	25	21	US-10-719-900-806438	Sequence 710757,
C	29	15	2.8	25	21	US-10-719-900-827771	Sequence 806438,
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C	56	15	2.8	47	16	US-10-051-681A-25	Sequence 25, App1
C	57	15	2.8	19	10	US-09-771-933-178	Sequence 178, App
C	58	15	2.8	19	10	US-10-871-222-319	Sequence 319, App
C	59	14	2.6	19	21	US-10-871-222-423	Sequence 423, App
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C	65	14	2.6	21	15	US-10-002-623-214	Sequence 214, App1
C	66	14	2.6	21	15	US-10-002-623-217	Sequence 217, App1
C	67	14	2.6	22	21	US-10-493-836-29	Sequence 29, App1
C	68	14	2.6	22	22	US-10-984-819-9	Sequence 9, App1
C	69	14	2.6	25	10	US-09-771-933-36	Sequence 36, App1
C	70	14	2.6	25	10	US-09-771-933-37	Sequence 37, App1
C	71	14	2.6	25	15	US-10-098-263B-62446	Sequence 62446, A
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93 14 2.6 25 21 US-10-719-900-475071 Sequence 475071,
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ALIGNMENTS

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844308
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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; Publication No. US20040005565A1
; GENERAL INFORMATION:
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; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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RESULT 3

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; Publication No. US20040005565A1
; GENERAL INFORMATION:
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; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
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; Publication No. US20050214823A1
; GENERAL INFORMATION:
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; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-79000
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DB 23 TGGCAGAGCTGGGATTC 7
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RESULT 5

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; Sequence 101784, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
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GenCore version 5.1.6
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Run on: October 7, 2005, 23:25:05 ; Search time 162.638 Seconds
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Title: US-09-887-941b-1

Perfect score: 530

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	2.8	25	4	US-09-396-196G-68144	Sequence 68144, A
5	2.8	41	2	US-08-857-946-92	Sequence 92, App1
6	2.8	41	3	US-08-970-740-92	Sequence 92, App1
7	2.6	15	1	US-08-363-240A-117	Sequence 117, App1
8	2.6	21	1	US-08-255-892-68	Sequence 68, App1
9	2.6	25	4	US-09-396-196G-94424	Sequence 94424, A
10	2.6	25	4	US-09-396-196G-94425	Sequence 94425, A
11	2.6	25	4	US-09-396-196G-115836	Sequence 115836, A
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ALIGNMENTS

RESULT 1

US-09-641-638-853/C
Sequence 853, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 853
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-529-376 : polymorphic base T or C
US-09-641-638-853

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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 171 CTCACAGAAAAGAG 186
DB 17 CTCACAGAAAAGAG 2

RESULT 2

US-10-170-097-853/C
Sequence 853, Application US/10170097
Patent No. 6794143
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GEN-T114XC2D1
CURRENT APPLICATION NUMBER: US/10/170,097
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304

SOFTWARE: Patent.pm
SEQ ID NO 853
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-529-376 : polymorphic base T or C
US-10-170-097-853

Query Match 3.0%; Score 16; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 CTCACAGAAAAGAG 186
DB 17 CTCACAGAAAAGAG 2

RESULT 3

US-09-396-196G-56102
Sequence 56102, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56102
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-56102

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Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 9 GGAGGGCACTCAGA 23

RESULT 4

US-09-396-196G-68144/C
Sequence 68144, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68144
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus

GenCore version 5.1.6
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Title: US-09-887-941B-1

Perfect score: 530

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Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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7: gb_est6:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                ALIGNMENTS

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DEFINITION      CA0A0047. mRNA sequence.
ACCESSION      AUI04142
VERSION      AUI04142.1      GI:13553663
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL
MEDLINE
PUBMED
COMMENT      Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
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Email: yusuzuki@ms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      35      GTGCTAGGCTGCAGAC      50

RESULT 2
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LOCUS      A2964788
DEFINITION      2M0234C1R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0234C11 R, genomic survey sequence.
ACCESSION      A2964788
VERSION      A2964788.1      GI:13836015
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL
COMMENT      plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000      Std Error: 0.00
Plate: 0234      row: C      column: 11
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 49.

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC2M0234C11"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      2.6%; Score 14; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      190      GTGAGAGACAGGAG      203
Db      16      GTGAGAGACAGGAG      29

RESULT 3
AUI04141      50 bp      mRNA      linear      EST 28-JAN-2004
LOCUS      AUI04141
DEFINITION      AUI04141 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP15203, mRNA sequence.
ACCESSION      AUI04141
VERSION      AUI04141.1      GI:13553662
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 557.336 Seconds
(without alignments)
5629.394 Million cell updates/sec

Title: US-09-887-941B-1
Perfect score: 530
Sequence: 1 cccgcgacctaacgacgacga.....ggaacatttagagagcccta 530

Scoring table: OLIGO NUC
Gapop_60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	17	3.2	20	12	ADH89628 Human Liv
3	16	3.0	17	3	AAFO2256 Hammethea
4	16	3.0	24	12	ADH56954 PCR prime
5	16	3.0	24	12	ADP48553 Chicken t
6	16	3.0	50	4	AAL31874 Human SNP
7	15	2.8	25	13	ADH31644 Small int
8	15	2.8	28	12	AA180178 Primer #1
9	15	2.8	28	12	ADP81947 Human NRI
10	15	2.8	37	3	AAZ99008 Slow upst
11	15	2.8	41	3	AAZ43351 Murine Ty
12	15	2.8	41	3	AAA05336 PCR prime
13	15	2.8	47	8	ABZ22300 Human D-a
14	15	2.8	47	9	AA160255 Human DAO
15	14	2.6	15	2	AA1749758 Human CET
16	14	2.6	19	4	AAH28653 Human int
17	14	2.6	20	4	AAH89418 Sense PCR
18	14	2.6	20	4	AAH28654 Human int
19	14	2.6	20	10	ABZ88331 Human oli
20	14	2.6	20	10	ABZ88332 Human oli

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24	14	2.6	21	9	ACH03502	Ach03502 Human lat
25	14	2.6	21	11	ADM65058	Adm65058 Human Y c
26	14	2.6	21	11	ADM65055	Adm65055 Human Y c
27	14	2.6	22	8	ACC47855	Acc47855 Rat elast
28	14	2.6	23	2	AAV48420	AAv48420 Tensiform
29	14	2.6	24	3	AAA96919	AAa96919 PCR prime
30	14	2.6	24	4	AAH77032	AaH77032 Human NF-
31	14	2.6	25	9	ACI12383	ACi12383 Human mic
32	14	2.6	25	9	ACI62455	ACi62455 Human mic
33	14	2.6	25	9	ACT63699	ACt63699 Human mic
34	14	2.6	25	9	ACT63699	ACt63699 Human mic
35	14	2.6	25	9	ACT63699	ACt63699 Human mic
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37	14	2.6	27	2	AAQ57222	AaQ57222 Enzymatic
38	14	2.6	27	2	AAQ57222	AaQ57222 Enzymatic
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C 95      13      2.5      18      2      AAG91959 T-cell Re
C 96      13      2.5      18      2      AAT92756 Vbeta20 T
C 97      13      2.5      18      2      AAT94252 Primer JB
C 98      13      2.5      18      2      AAX86621 Sonic hed
C 99      13      2.5      18      4      AAH23358 Nucleotid
C 100     13      2.5      18      6      AAS14344 3'-PCR pr
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ALIGNMENTS

RESULT 1

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XX
AC ADH89551;
XX
DT 22-APR-2004 (first entry)
XX
DE Human Livin antisense oligonucleotide ISIS 205802.
XX
KW hyperproliferative disorder; aberrant apoptosis; human; ss; Livin;
XX antisense.
XX
OS Homo sapiens.
XX Synthetic.
XX
PN US2004005565-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00188646.
XX
PR 02-JUL-2002; 2002US-00188646.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX
DR WPI; 2004-098436/10.
XX
PT New antisense oligonucleotide, having a sequence targeted to a nucleic
XX acid encoding Livin, useful for preparing a composition for treating
XX hyperproliferative disorder or aberrant apoptosis.
XX
PS Example 15; SEQ ID NO 20; 60pp; English.
XX
CC The invention relates to an antisense oligonucleotide targeted to a
XX nucleic acid encoding Livin and that specifically hybridizes with the
XX nucleic acid encoding Livin and inhibits expression of Livin. The
XX antisense oligonucleotide is useful for preparing a composition for
XX treating hyperproliferative disorder or aberrant apoptosis. The present
XX sequence represents a human livin antisense oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 3.2%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 43 AAGTGCAGAGCTGGGA 59
Db 1 AAGTGCAGAGCTGGGA 17
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RESULT 2
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XX ADH89628 standard; DNA; 20 BP.
XX
AC ADH89628;
XX
DT 22-APR-2004 (first entry)
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XX
DE Human Livin target region ISIS 123462.
XX
KW hyperproliferative disorder; aberrant apoptosis; human; ss; Livin.
XX
OS Homo sapiens.
XX
PN US2004005565-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00188646.
XX
PR 02-JUL-2002; 2002US-00188646.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX
DR WPI; 2004-098436/10.
XX
DE New antisense oligonucleotide, having a sequence targeted to a nucleic
XX acid encoding Livin, useful for preparing a composition for treating
XX hyperproliferative disorder or aberrant apoptosis.
XX
PS Example 15; SEQ ID NO 97; 60pp; English.
XX
CC The invention relates to an antisense oligonucleotide targeted to a
XX nucleic acid encoding Livin and that specifically hybridizes with the
XX nucleic acid encoding Livin and inhibits expression of Livin. The
XX antisense oligonucleotide is useful for preparing a composition for
XX treating hyperproliferative disorder or aberrant apoptosis. The present
XX sequence represents a human livin target region.
XX
SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
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Query Match 3.2%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 20 AAGTGCAGAGCTGGGA 4
XX
RESULT 3
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XX
AC AAF02256;
XX
DT 16-FEB-2001 (first entry)
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DE Hammerhead ribozyme substrate #551.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mswiggen U;
XX
DR WPI; 2000-647423/62.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 3251.98 Seconds
(without alignment)
7897.122 Million cell updates/sec

Title: US-09-887-941B-1
Perfect score: 530
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Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_htg:.*
3: gb_in:.*
4: gb_om:.*
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7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_ste:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 4	15	2.8	41	6	AR089810
C 5	15	2.8	45	9	HS4224269
C 6	15	2.8	47	6	AX741678
C 7	15	2.8	47	6	AX776500
C 8	14	2.6	21	6	A32743
C 9	14	2.6	21	6	I84297
C 10	14	2.6	23	6	A87861
C 11	14	2.6	23	6	A89828
C 12	14	2.6	23	6	BD065374
C 13	14	2.6	27	6	I37005
C 14	14	2.6	27	6	I93855
C 15	14	2.6	27	6	AR242663
C 16	14	2.6	27	6	AX317187
C 17	14	2.6	27	6	AX555913
C 18	14	2.6	31	6	I37152
C 19	14	2.6	31	6	I37153

C 20	14	2.6	31	6	I37154	I37154 Sequence 16
C 21	14	2.6	31	6	I94002	I94002 Sequence 16
C 22	14	2.6	31	6	I94003	I94003 Sequence 16
C 23	14	2.6	31	6	I94004	I94004 Sequence 16
C 24	14	2.6	35	6	CO814987	CO814987 Sequence
C 25	14	2.6	36	10	MMTCR48	MMTCR48 Sequence
C 26	14	2.6	50	6	CO858049	CO858049 Sequence
C 27	13	2.5	15	6	AR180156	AR180156 Sequence
C 28	13	2.5	16	6	A18727	A18727 kozak conse
C 29	13	2.5	17	6	AR434372	AR434372 Sequence
C 30	13	2.5	17	6	AR434373	AR434373 Sequence
C 31	13	2.5	17	6	AR434374	AR434374 Sequence
C 32	13	2.5	17	6	AR434375	AR434375 Sequence
C 33	13	2.5	17	6	AR434376	AR434376 Sequence
C 34	13	2.5	17	6	AX737603	AX737603 Sequence
C 35	13	2.5	18	6	A26383	A26383 probe no.1.
C 36	13	2.5	18	6	AR060406	AR060406 Sequence
C 37	13	2.5	18	6	AR128964	AR128964 Sequence
C 38	13	2.5	18	6	I65329	I65329 Sequence 51
C 39	13	2.5	18	6	AR534202	AR534202 Sequence
C 40	13	2.5	18	6	AR534203	AR534203 Sequence
C 41	13	2.5	18	6	AX202658	AX202658 Sequence
C 42	13	2.5	19	6	AR295829	AR295829 Sequence
C 43	13	2.5	19	6	AX394639	AX394639 Sequence
C 44	13	2.5	20	6	BD228522	BD228522 IL-17 hom
C 45	13	2.5	20	6	AR183227	AR183227 Sequence
C 46	13	2.5	20	6	AR234630	AR234630 Sequence
C 47	13	2.5	20	6	AR262248	AR262248 Sequence
C 48	13	2.5	20	6	AR359747	AR359747 Sequence
C 49	13	2.5	20	6	AX149139	AX149139 Sequence
C 50	13	2.5	20	6	AX281333	AX281333 Sequence
C 51	13	2.5	20	6	AX342562	AX342562 Sequence
C 52	13	2.5	20	6	AX347474	AX347474 Sequence
C 53	13	2.5	20	6	AX402789	AX402789 Sequence
C 54	13	2.5	21	6	AR296505	AR296505 Sequence
C 55	13	2.5	21	6	AR567769	AR567769 Sequence
C 56	13	2.5	22	6	AR068025	AR068025 Sequence
C 57	13	2.5	22	6	AR120228	AR120228 Sequence
C 58	13	2.5	22	6	AR179906	AR179906 Sequence
C 59	13	2.5	22	6	AR182279	AR182279 Sequence
C 60	13	2.5	22	6	AR371883	AR371883 Sequence
C 61	13	2.5	22	6	AX718077	AX718077 Sequence
C 62	13	2.5	22	6	BD017061	BD017061 Novel pol
C 63	13	2.5	22	6	BD088974	BD088974 A method
C 64	13	2.5	23	6	AX004025	AX004025 Sequence
C 65	13	2.5	24	6	AR069189	AR069189 Sequence
C 66	13	2.5	24	6	AR102700	AR102700 Sequence
C 67	13	2.5	24	6	I64407	I64407 Sequence 23
C 68	13	2.5	24	6	AR183228	AR183228 Sequence
C 69	13	2.5	24	6	AR228157	AR228157 Sequence
C 70	13	2.5	24	6	AR364575	AR364575 Sequence
C 71	13	2.5	24	6	AX289764	AX289764 Sequence
C 72	13	2.5	24	6	BD015755	BD015755 Estrogen
C 73	13	2.5	25	6	AR158396	AR158396 Sequence
C 74	13	2.5	25	6	AR158397	AR158397 Sequence
C 75	13	2.5	25	6	AR158398	AR158398 Sequence
C 76	13	2.5	25	6	AR158399	AR158399 Sequence
C 77	13	2.5	25	6	AR158400	AR158400 Sequence
C 78	13	2.5	25	6	AR158401	AR158401 Sequence
C 79	13	2.5	25	6	AR158402	AR158402 Sequence
C 80	13	2.5	25	6	AR158403	AR158403 Sequence
C 81	13	2.5	25	6	AR158404	AR158404 Sequence
C 82	13	2.5	25	6	AR158405	AR158405 Sequence
C 83	13	2.5	25	6	AR158406	AR158406 Sequence
C 84	13	2.5	25	6	AR158407	AR158407 Sequence
C 85	13	2.5	25	6	AR158408	AR158408 Sequence
C 86	13	2.5	25	6	CO864140	CO864140 Sequence
C 87	13	2.5	25	6	CO864141	CO864141 Sequence
C 88	13	2.5	25	6	CO864142	CO864142 Sequence
C 89	13	2.5	25	6	CO875206	CO875206 Sequence
C 90	13	2.5	25	6	AR435187	AR435187 Sequence
C 91	13	2.5	25	6	AR435188	AR435188 Sequence
C 92	13	2.5	25	6	AR435189	AR435189 Sequence

c 93 13 2.5 25 6 AR435190
 c 94 13 2.5 25 6 AR435191
 c 95 13 2.5 25 6 AR435192
 c 96 13 2.5 25 6 AR435193
 c 97 13 2.5 25 6 AR435194
 c 98 13 2.5 25 6 AR435195
 c 99 13 2.5 25 6 AR435196
 c 100 13 2.5 25 6 AR435197

ALIGNMENTS

RESULT 1
 BD254454/c 17 bp DNA linear PAT 17-JUL-2003
 LOCUS
 DEFINITION Regulation of repressor genes using nucleic acid molecules.
 ACCESSION BD254454
 VERSION BD254454.1 GI:33064224
 KEYWORDS JP 2002541795-A/2247.
 SOURCE unidentitied
 ORGANISM unidentitied.
 unclassified.

REFERENCE
 AUTHORS Blact,L., Zwick,M., Pavco,P. and Mcswiggen,J.
 TITLE Regulation of repressor genes using nucleic acid molecules
 JOURNAL Patent: JP 2002541795-A 2247 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Eukaryote
 PN JP 2002541795-A/2247
 PD 10-DEC-2002
 PF 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/123390
 P1 LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC
 C12P21/02,

PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
 C12R1:91)
 PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
 PC A61K37/02,
 PC (C12N5/00,C12R1:91)
 CC Regulation of repressor genes using nucleic acid molecules FH
 Key Location/Qualifiers
 FT source 1..17
 Location/Qualifiers
 1..17
 /organism="Eukaryote".
 /organism="unidentitied"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 3.0%; Score 16; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GGCTGCAGACGCTT 481
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 Db 16 GGCTGCAGACGCTT 1

RESULT 2
 CQ006442 50 bp DNA linear PAT 16-JAN-2004
 LOCUS
 DEFINITION Sequence 5082 from Patent WO0147944.
 ACCESSION CQ006442
 VERSION CQ006442.1 GI:41013074
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Shinkens,R.A. and Leach,M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0147944-A 5082 05-JUL-2001;
 Curing Corporation (US)
 FEATURES Location/Qualifiers
 source 1..50
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 misc_feature 25..26
 /note="Nucleotide deleted between bases 25 and 26
 Accession number C943972159"

ORIGIN

Query Match 3.0%; Score 16; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GGCGCCAGACCA 326
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 Db 27 GGCGCCAGACCA 42

RESULT 3
 CQ866809 28 bp DNA linear PAT 10-SEP-2004
 LOCUS
 DEFINITION Sequence 27 from Patent WO2004054601.
 ACCESSION CQ866809
 VERSION CQ866809.1 GI:51987754
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 Other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Weise,M., Eulenberger,K., Molitor,A., Steuernagel,A., Nguyen,T. and
 Katerle,Y.
 TITLE Fwd, ppc1, adk3, cg3860, cdk4, cg7134, eip75b involved in the
 regulation of energy homeostasis
 JOURNAL Patent: WO 2004054601-A 27 01-JUL-2004;
 Develogen Aktiengesellschaft fuer entwicklungsbiologische Forschung
 (DE)
 Location/Qualifiers
 source 1..28
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: PCR
 primer-human NR1D1 Tagman probe primer; 5'(5/6-FAM) and
 3'(5/6-TAMRA)"

ORIGIN

Query Match 2.8%; Score 15; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 CAGACGCTTGCCA 485
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 Db 14 CAGACGCTTGCCA 28

RESULT 4
 AR089810 41 bp DNA linear PAT 07-SEP-2000
 LOCUS
 DEFINITION Sequence 92 from patent US 5994075.
 ACCESSION AR089810
 VERSION AR089810.1 GI:10016565
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 41)